

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:12 ; Search time 50.5 Seconds  
(without alignments)  
615.450 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583

Sequence: 1 APPVAGGSPSWZLFPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	566.5	97.2	462	2 AAW14933	Aaw14933 2A2 (Chim
2	566.5	97.2	462	2 AAW14934	Aaw14934 2A2 (Chim
3	566.5	97.2	463	2 AAW14939	Aaw14939 3F4 (Chim
4	566.5	97.2	463	2 AAW14940	Aaw14940 3F4 (Chim
5	566.5	97.2	472	5 ABP51695	Abp51695 5G1.i-TPO
6	565	96.9	110	2 AAR41717	Aar41717 Undefined
7	565	96.9	218	3 AAB07478	Aab07478 Amino aci
8	565	96.9	218	4 AAB76425	Aab76425 Human IgG
9	565	96.9	218	4 AAB67205	Aab67205 Human IgG
10	565	96.9	218	5 AAG78436	Aag78436 Native se
11	565	96.9	218	5 ABR42442	Abr42442 Human IgG
12	565	96.9	229	7 ADD32013	Add32013 Heterolog
13	565	96.9	284	6 AAE30927	Aae30927 Glyc8-Glu2
14	565	96.9	327	2 AAW37346	Aaw37346 Immunoglo
15	565	96.9	327	5 AAM47859	Aam47859 Human Ig-
16	565	96.9	327	6 AAE32318	Aae32318 Human imm
17	565	96.9	327	6 AAE32830	Aae32830 Human imm
18	565	96.9	327	6 AAO30892	Aao30892 Human imm
19	565	96.9	329	2 AAW70801	Aaw70801 Amino aci
20	565	96.9	329	3 AAY92190	Aay92190 Human IgG
21	565	96.9	330	6 ABR42735	Abr42735 Anti-tiss
22	565	96.9	382	2 AAR90922	Aar90922 IL4.Y124D
23	565	96.9	382	2 AAR90921	Aar90921 IL4.Y124D
24	565	96.9	396	2 AAW10534	Aaw10534 Leptin 1-
25	565	96.9	396	2 AAW10535	Aaw10535 Leptin 1-

26	565	96.9	403	7 ADD32018	Add32018 Heterolog
27	565	96.9	432	2 AAY17903	Aay17903 Human IFN
28	565	96.9	433	2 AAW18579	Aaw18579 Interfero
29	565	96.9	443	2 AAW13564	Aaw13564 Humanised
30	565	96.9	444	2 AAY31672	Aay31672 Human IgG
31	565	96.9	444	6 ABR55342	Abr55342 Amino aci
32	565	96.9	444	7 ADC73234	Adc73234 Protein s
33	565	96.9	450	6 ABP96294	Abp96294 4AS-3.1.1
34	565	96.9	463	2 AAW14932	Aaw14932 Murine an
35	565	96.9	463	2 AAW14935	Aaw14935 2A2 Human
36	565	96.9	464	2 AAW14941	Aaw14941 3F4 Human
37	565	96.9	464	2 AAW14938	Aaw14938 Murine an
38	565	96.9	465	7 ADD93783	Add93783 Monoclonal
39	565	96.9	467	2 AAR80617	Aar80617 Anti-huma
40	565	96.9	467	2 AAW14927	Aaw14927 Human gam
41	565	96.9	467	2 AAW14925	Aaw14925 Human gam
42	565	96.9	467	2 AAW14926	Aaw14926 Human gam
43	565	96.9	467	7 ADE31591	Ade31591 Gamma 4 h
44	565	96.9	467	7 ADE31593	Ade31593 Gamma 4 h
45	565	96.9	467	7 ADE31589	Ade31589 Gamma 4 h

#### ALIGNMENTS

RESULT 1  
AAW14933  
ID AAW14933 standard; protein; 462 AA.  
XX  
AC AAW14933;  
XX  
DT 17-OCT-2003 (revised)  
DT 16-JUN-1997 (first entry)  
XX  
DE 2A2 (Chimeric) human G2/G4 chimeric antibody.  
XX  
KW Xenotransplantation; graft rejection; cell interaction; pig;  
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
KW chimeric antibody; diagnosis.  
XX  
XX Homo; sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
PN WO9711971-A1.  
XX  
PD 03-APR-1997.  
XX  
PF 27-SEP-1996; 96WO-US015575.  
XX  
PR 28-SEP-1995; 95US-0004489P.  
PR 26-SEP-1996; 96US-00004489.  
XX  
PA (ALEX-) ALEXION PHARM INC.  
XX  
PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;  
XX  
XX WPI; 1997-212855/19.  
DR N-ESDB; AAT62931.  
XX  
PT Antibodies binding to porcine but not human cell interaction proteins -  
PT useful to treat and assay for rejection of xenografted porcine organs,  
PT tissues or cells.  
XX  
PS Disclosure; Page 42-44, 105pp; English.  
XX  
CC A chimeric antibody (AAW14933) comprises the C1 and hinge regions of  
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a  
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)  
CC monoclonal antibody (MAb) 2A2 heavy chain variable region sequence (see  
CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is  
CC useful for diagnosing human rejection of porcine xenotransplants and for  
CC improving xenotransplantation of porcine cells, tissues and organs into

CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 462 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 462;

Best Local Similarity 99.1%; Pred. No. 1.2e-48;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 247 APPVA-GPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 305

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAK 110

DB 306 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAK 355

#### RESULT 2

AAW14934  
ID AAW14934 standard; protein; 462 AA.

XX AAW14934;

AC AAW14934;

DT 17-OCT-2003 (revised)

DT 16-JUN-1997 (first entry)

XX 2A2 (Chimeric) human G2/G4 chimeric antibody.

XX Xenotransplantation; graft rejection; cell interaction; pig;

XX vascular cell adhesion molecule; VCAM; monoclonal antibody;

XX chimeric antibody; diagnosis.

XX Homo; sapiens.

OS Mus sp.

OS Chimeric.

XX WO9711971-AL.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.

XX 26-SEP-1996; 96US-00004489.

XX (ALEX-) ALEXION PHARM INC.

XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;

XX WPI; 1997-212855/19.

XX N-PSDB; AAT62932.

XX Antibodies binding to porcine but not human cell interaction proteins -

XX useful to treat and assay for rejection of xenografted porcine organs,

XX tissues or cells.

XX Disclosure; Page 44-47; 105pp; English.

XX A chimeric antibody (AAW14934) comprises the C1 and hinge regions of

XX human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a

XX murine anti-porcine soluble vascular cell adhesion molecule (VCAM)

XX monoclonal antibody (MAb) 2A2 heavy chain variable region sequence (see

XX also AAW14932). The chimeric antibody is specific for porcine VCAM. It is

XX useful for diagnosing human rejection of porcine xenotransplants and for

XX improving xenotransplantation of porcine cells, tissues and organs into

XX human recipients. (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 462 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 462;

Best Local Similarity 99.1%; Pred. No. 1.2e-48;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 247 APPVA-GPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 305

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAK 110

DB 306 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAK 355

#### RESULT 3

AAW14939  
ID AAW14939 standard; protein; 463 AA.

XX AAW14939;

DT 17-OCT-2003 (revised)

DT 16-JUN-1997 (first entry)

XX 3P4 (Chimeric) human G2/G4 chimeric antibody.

XX Xenotransplantation; graft rejection; cell interaction; pig;

XX vascular cell adhesion molecule; VCAM; monoclonal antibody;

XX chimeric antibody; diagnosis.

XX Homo; sapiens.

OS Mus sp.

OS Chimeric.

XX WO9711971-AL.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.

XX 26-SEP-1996; 96US-00004489.

XX (ALEX-) ALEXION PHARM INC.

XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;

XX WPI; 1997-212855/19.

XX N-PSDB; AAT62932.

XX Antibodies binding to porcine but not human cell interaction proteins -

XX useful to treat and assay for rejection of xenografted porcine organs,

XX tissues or cells.

XX Disclosure; Page 56-57; 105pp; English.

XX A chimeric antibody (AAW14939) comprises the C1 and hinge regions of

XX human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a

XX murine anti-porcine soluble vascular cell adhesion molecule (VCAM)

XX monoclonal antibody (MAb) 3P4 heavy chain variable region sequence (see

XX also AAW14938). The chimeric antibody is specific for porcine VCAM. It is

XX useful for diagnosing human rejection of porcine xenotransplants and for

XX improving xenotransplantation of porcine cells, tissues and organs into

XX human recipients. (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 463 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 463;

Best Local Similarity 99.1%; Pred. No. 1.2e-48;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 248 APPVA-GPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 306

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAK 110

DB 307 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAK 356

## RESULT 4

AAW14940  
ID AAW14940 standard; protein; 463 AA.  
XX  
AC AAW14940;  
XX  
DT 17-OCT-2003 (revised)  
DT 16-JUN-1997 (first entry)  
XX  
XX 3F4 (Chimeric) human G2/G4 chimeric antibody.

XX Xenotransplantation; graft rejection; cell interaction; pig;  
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
KW Chimeric antibody; diagnosis.  
XX  
OS Homo; sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
XX WO9711971-A1.  
XX  
XX 03-APR-1997.  
XX  
XX 27-SEP-1996; 96WO-US015575.  
XX  
XX 28-SEP-1995; 95US-0004489P.  
PR 26-SEP-1996; 96US-00004489.  
XX  
XX (ALEX-) ALEXION PHARM INC.  
XX  
XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;  
XX WPI; 1997-212855/19.  
XX N-PSDB; AAT62937.  
XX  
XX Antibodies binding to porcine but not human cell interaction proteins -  
XX useful to treat and assay for rejection of xenografted porcine organs,  
XX tissues or cells.

Disclosure; Page 58-61; 105pp; English.

XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of  
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a  
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM) and a  
CC monoclonal antibody (Mab) 3F4 heavy chain variable region sequence (see  
CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is  
CC useful for diagnosing human rejection of porcine xenotransplants and for  
CC improving xenotransplantation of porcine cells, tissues and organs into  
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)  
XX  
XX Sequence 463 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 463;

Best Local Similarity 99.1%; Pred. No. 1.2e-48;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDILMSRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 60

DB 248 APPVA-GPSVFLPPPKDILMSRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 306

QY 61 PREQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110

DB 307 PREQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 356

## RESULT 5

ABP51695  
ID ABP51695 standard; protein; 472 AA.  
XX  
XX  
XX ABP51695;  
XX  
DT 01-OCT-2002 (first entry)

XX

DE

XX

KW

KW

KW

XX

OS

OS

XX

PN

XX

PD

XX

PF

XX

PR

PR

PR

XX

XX

PA

XX

PI

XX

XX

DR

DR

XX

PT

PT

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 472 AA;

Query Match

Best Local Similarity 97.2%; Score 566.5; DB 5; Length 472;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDILMSRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 60

DB 257 APPVA-GPSVFLPPPKDILMSRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 315

QY 61 PREQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110

DB 316 PREQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 365

RESULT 6

5G1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.

TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;  
complementarity determining region; immunoglobulin; antianaemic;  
haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

Homo sapiens.

Synthetic.

WO200246238-A2.

13-JUN-2002.

05-DEC-2001; 2001WO-US047656.

05-DEC-2000; 2000US-0251448P.

04-MAY-2001; 2001US-0288889P.

29-MAY-2001; 2001US-0294068P.

(ALEX-) ALEXION PHARM INC.

Bowdish KS, Barbas-Frederickson S, Renshaw M;

WPI; 2002-566610/60.

N-PSDB; ABQ73374.

A novel immunogen molecule comprising a region in which amino acid

residues corresponding to at least a portion of the complementary

determining region are replaced or fused with an erythropoietin or

thrombopoietin mimetic.

Example 4; Fig 13A; 113pp; English.

The present invention describes an immunoglobulin molecule or its fragment

(I) comprising a region where amino acid residues corresponding to at

least a portion of the complementary determining region (CDR) are

replaced or fused with biologically active peptides e.g. a peptide

mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,

that is flanked with proline at its carboxy terminus. (I) has

antianaemic, haemostatic and nephrotropic activities, and can be used as

a stimulator of proliferation, differentiation and maturation of

haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful

for stimulating proliferation, differentiation or growth of

promegakaryocytes or megakaryocytes, where (I) is contacted with

promegakaryocytes or megakaryocytes, which results in increased platelet

production. (I) with a region where amino acid residues corresponding to

a portion of CDR is replaced with an EPO mimetic, or which has one or

more of its CDRs fused to an EPO mimetic, is useful for increasing the

production of red blood cells, where (I) is contacted with haematopoietic

stem cells or their progenitors. (I) is useful for diagnostics or

therapeutics, in cell isolation strategies, and for treating patients

suffering from deficiency in cell populations caused by disease,

disorders or treatments related to the suppression of haematopoiesis.

ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in

the exemplification of the present invention

AAR41717  
ID AAR41717 standard; protein; 110 AA.  
XX  
XX AAR41717;  
AC  
XX  
DT 20-OCT-2000 (first entry)  
XX  
DE 25-MAR-2003 (revised)  
DF 20-OCT-1993 (first entry)  
XX  
XX Undefined ORF2 encoded by plasmid pAH4808.  
DE  
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;  
KW light; chain; variable; constant; region; anti-human; pAH4807;  
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;  
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;  
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;  
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.  
XX  
XX Synthetic.  
CS  
XX WO9310819-A1.  
XX  
XX 10-JUN-1993.  
XX  
XX 24-NOV-1992; 92WO-US010206.  
XX  
XX 26-NOV-1991; 91US-00800458.  
XX  
XX (ALKE-) ALKERMES INC.  
XX  
XX Frieden PM;  
XX  
XX WPI; 1993-196742/24.  
DR N-PSDB; AAQ43848.  
DR  
XX Antibody conjugates specific for transferrin receptor - used for  
PT diagnosis and treatment of cancer, AIDS and neurological disorders.  
PT  
XX Disclosure; Fig 193; 151pp; English.  
PS  
XX The sequences given in AAR41715-18 are encoded by the expression vector  
XX pAH4808. This vector represents the cloning of the human gamma isotype,  
CC gamma-4, with the variable region of the murine monoclonal antibody  
CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the  
CC heavy chain (VH) is derived from a murine source and the sequences  
CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,  
CC in combination with the chimeric light chain vector, pA4611 (see also  
CC AAQ43845), was transfected into SP2/0 cells and clones were isolated.  
CC 128.1 is an anti-human transferrin receptor antibody which binds to the  
CC transferrin receptor on brain capillary endothelial cells. This antibody  
CC may be used in a conjugate in which it is linked to a neuropharmaceutical  
CC or diagnostic agent. The conjugate may be used to treat or prevent  
CC neurological disorders eg. Brain tumours, AIDS, stroke, epilepsy,  
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 110 AA;  
SQ  
Query Match 96.9%; Score 565; DB 2; Length 110;  
Best Local Similarity 97.3%; Pred. No. 3.le-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60  
DB 1 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60  
QY 61 PREQFNSTYRVSVLTVHLQDNLNGKEYCKVSNKGLPSSIEKTSKAK 110  
DB 62 PREQFNSTYRVSVLTVHLQDNLNGKEYCKVSNKGLPSSIEKTSKAK 111  
RESULT 7  
AAB07478  
ID AAB07478 standard; protein; 218 AA.  
XX  
XX AAB07478;  
AC  
XX 20-OCT-2000 (first entry)  
XX  
DE Amino acid sequence of native IgG Fc region hum1G4.  
DF  
XX IgG antibody; light chain; Fc region; effector function; cancer; allergy;  
KW asthma; LFA-1-mediated disorder; tumour; cancer.  
XX  
XX Homo sapiens.  
OS  
XX WO200042072-A2.  
PN  
XX 20-JUL-2000.  
PD  
XX 14-JAN-2000; 2000WO-US000973.  
PF  
XX 15-JAN-1999; 99US-0116023P.  
PR  
XX (GETH ) GENENTECH INC.  
PA  
XX Presta LG;  
PI  
XX WPI; 2000-476035/41.  
DR  
XX New Fc region-containing polypeptides that have altered effector function  
PT due to one or more amino acid modifications in the Fc region, useful in  
PT the treatment of cancer and allergic conditions such as asthma.  
PT  
XX Disclosure; Fig 22A; 132pp; English.  
PS  
XX AAB07474-78 represent native IgG Fc regions. The proteins are used to  
XX produce Fc region-containing polypeptides that have altered effector  
CC function as a consequence of one or more amino acid modifications in the  
CC Fc region. The variant polypeptides are useful for treating cancer, and  
CC allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1  
CC -mediated disorders. Where the polypeptide binds the HER2 receptor, the  
CC disorder preferably is HER2-expressing cancer, e.g. a benign or malignant  
CC tumour characterized by overexpression of the HER2 receptor. Such cancers  
CC include breast cancer, squamous cell cancer, small-cell lung cancer, non-  
CC small cell lung cancer, gastrointestinal cancer, pancreatic cancer, heptatoma,  
CC glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,  
CC colon cancer, colorectal cancer, endometrial carcinoma, salivary gland  
CC carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,  
CC thyroid cancer, hepatic carcinoma and various types of head and neck  
CC cancer  
XX  
XX Sequence 218 AA;  
SQ  
Query Match 96.9%; Score 565; DB 3; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.9e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60  
DB 2 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 61  
QY 61 PREQFNSTYRVSVLTVHLQDNLNGKEYCKVSNKGLPSSIEKTSKAK 110  
DB 62 PREQFNSTYRVSVLTVHLQDNLNGKEYCKVSNKGLPSSIEKTSKAK 111  
RESULT 8  
AAB76425  
ID AAB76425 standard; protein; 218 AA.  
XX  
XX AAB76425;  
AC  
XX 10-APR-2001 (first entry)  
DT  
XX Human IgG4 Fc region amino acid sequence.  
DE  
XX

KW Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;  
KW metabolic disorder; nutritional deficiency; Alzheimer's disease;  
KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;  
KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.  
XX Homo sapiens.  
XX WO200101748-A2.  
XX PD 11-JAN-2001.  
XX 30-JUN-2000; 2000WO-US018283.  
XX 02-JUL-1999; 98US-01422322.  
XX (GETH ) GENENTECH INC.  
XX PA Dennis MS;  
XX PI WPI; 2001-123048/13.  
XX DR Non-naturally occurring peptide ligands which compete for binding human  
XX erB2 gene products, useful for treating e.g. Alzheimer's disease,  
XX multiple sclerosis and diabetic neuropathy.  
XX PS Disclosure; Fig 2A; 116pp; English.  
XX CC This invention relates to non-naturally occurring peptide ligands which  
XX bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides  
XX represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples  
XX of the ErbB2 binding ligands of the invention. Sequences AAB76421 -  
XX AAB76431 represent antibody Fc amino acid sequences used in the isolation  
XX of the peptides of the invention. The peptides compete for binding ErbB2  
XX with naturally occurring ligands, and may be used to treat disorders  
XX characterized by over expression of HER2/ErbB2 such as cancers, diseases  
XX of the nervous system, musculature and epithelia, e.g. nervous system  
XX damage resulting from trauma, surgery, strokes, ischaemia, infection,  
XX metabolic disorders, nutritional deficiency or toxic agents. In  
XX particular the synthetic peptide ligands may be used to treat Alzheimer's  
XX disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's  
XX chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy  
XX associated with diabetes  
XX Sequence 218 AA;  
SQ Query Match 96.9%; Score 565; DB 4; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.9e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPPKDITLMIISTPTVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTK 60  
DB 2 APEFLGGSPVFLPPPKDITLMIISTPTVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTK 61  
QY 61 PREQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110  
DB 62 PREQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 111  
RESULT 9  
AAB67205  
ID AAB67205 standard; protein; 218 AA.  
AC AAB67205;  
XX 10-APR-2001 (first entry)  
XX Human IgG4.  
XX Fusion protein; immunoglobulin; multidimerization domain; ligand.  
XX Homo sapiens.  
XX WO200102440-A1.  
PN

XX 11-JAN-2001.  
XX 30-JUN-2000; 2000WO-US018185.  
XX 02-JUL-1999; 99US-0142088P.  
XX (GETH ) GENENTECH INC.  
XX PI Dennis MS, Lazarus RA;  
XX WPI; 2001-123106/13.  
XX Novel fusion polypeptides comprising a peptide ligand domain which  
XX functions to target hybrid molecule to target cell, and immunoglobulin  
XX constant region multimerization domain.  
XX Disclosure; Fig 2; 69pp; English.  
XX CC The present invention relates to a fusion protein, comprising a peptide  
XX ligand and an immunoglobulin (Ig) constant region multimerization domain  
XX (ib). The hybrid molecules comprising the peptide ligands and their  
XX functional derivatives can be used in the same applications as, a peptide  
XX ligand can be used. For example the peptide ligand can bind ErbB2. The  
XX peptide ligand may bind to and inhibit the activity associated with a  
XX particular target molecule  
XX Sequence 218 AA;  
SQ Query Match 96.9%; Score 565; DB 4; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.9e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPPKDITLMIISTPTVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTK 60  
DB 2 APEFLGGSPVFLPPPKDITLMIISTPTVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTK 61  
QY 61 PREQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110  
DB 62 PREQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 111  
RESULT 10  
AAG78436  
ID AAG78436 standard; protein; 218 AA.  
AC AAG78436;  
XX 12-APR-2002 (first entry)  
XX Native sequence human IgG Fc region sequence humIgG4.  
XX Antibody; antigen; immunoglobulin; ADCC; CDC; anti-globin response;  
XX antibody dependant cell mediated cytotoxicity;  
XX complement dependant cytotoxicity; epidermal growth factor receptor;  
XX tumour necrosis factor; lymphocyte; tetraivalent antibody; cytostatic;  
XX antiinflammatory; antipsoriatic; dermatological; antitumor;  
XX antiasthmatic; antiarteriosclerotic; antirheumatic; antibacterial;  
XX antiarthritic; neuroprotective; immunosuppressive; antianaemic;  
XX antiallergic; antidiabetic; gene therapy; human.  
XX Homo sapiens.  
XX WO200177342-A1.  
XX 18-OCT-2001.  
XX 20-MAR-2001; 2001WO-US008928.  
XX 11-APR-2000; 2000US-0195819P.  
XX (GETH ) GENENTECH INC.  
XX

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PI Miller KL, Presta LG;
XX WPI; 2002-049149/06.
XX
XX Novel engineered antibody useful in therapeutic applications, contains a
XX dimerization domain and three or more antigen binding sites.
XX
XX Disclosure; Fig 3; 186pp; English.
XX
XX This invention relates to an isolated antibody comprising a dimerisation
XX domain and three or more antigen binding sites amino-terminal to the
XX domain. It is cytostatic, antiinflammatory, antibacterial,
XX immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used
XX in gene therapy. Along with a cytotoxic agent, is useful for treating a
XX disorder e.g. cancer in a mammal, for inducing apoptosis of a cancer
XX cell, and for killing a B cell or a cell which overexpresses or expresses
XX an ErbB receptor and for treating benign and malignant tumours,
XX inflammatory, angiogenic and immunological disorders, autoimmune
XX diseases, central nervous system inflammatory disorders. The antibody is
XX also useful for immunodiagnosis of various diseases including cancer, for
XX human therapy in redirected cytotoxicity, and also useful as fibrinolytic
XX agents or vaccine adjuvants, useful as affinity purification agent, in
XX diagnostic assays for detecting the expression of antigen of interest in
XX specific cells, tissue or serum, and useful for blocking an immune
XX response to a foreign antigen. The antigen is internalised faster than a
XX bivalent antibody by a cell expressing an antigen to which the antibodies
XX bind. The antibody comprises three or four heavy chain variable domains
XX which are able to combine with three or four light chain variable domain
XX polypeptides to form three or four antigen binding sites directed against
XX the same antigen. This sequence represents the native sequence human IgG
XX Fc region, humiG4
XX
XX Sequence 218 AA;
XX
XX Query Match 96.9%; Score 565; DB 5; Length 218;
XX Best Local Similarity 97.3%; Pred. No. 6.9e-49;
XX Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVGFNNYVVGVEVHNATK 60
XX DB 2 APEFLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVGFNNYVVGVEVHNATK 61
XX
XX QY 61 PREQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
XX DB 62 PREQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 111
XX
XX RESULT 11
XX ABR42442
XX ID ABR42442 standard; protein; 218 AA.
XX AC ABR42442;
XX DT 11-AUG-2003 (first entry)
XX DE Human IgG4 Fc region.
XX KW Human; antibody; IgG4; cytostatic; immunosuppressive; antiinflammatory;
XX RW antimicrobial.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 153
XX /note= "given as 'Z' in Fig 23"
XX
XX WO2003035835-A2.
XX
XX 01-MAY-2003.
XX
XX 22-OCT-2002; 2002WO-US033739.
XX
XX 25-OCT-2001; 2001US-0337642P.

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PR 09-JAN-2002; 2002US-0347694P.
XX (GETH ) GENENTECH INC.
XX Presta LG;
XX WPI; 2003-421411/39.
XX
XX New composition comprising a glycoprotein having a Fc region useful for
XX treating cancer, autoimmune disease, inflammatory disorder or infection
XX in a mammal.
XX
XX Disclosure; Fig 23; 139pp; English.
XX
XX The present sequence is the protein sequence of the Fc region of human
XX IgG4. A claimed composition comprises a glycoprotein having a Fc region.
XX About 80-100% of the glycoprotein comprises a mature core carbohydrate
XX structure which lacks fucose attached to the Fc region. The glycoprotein
XX preferably comprises an antibody, and the Fc region is preferably a human
XX IgG Fc region, especially a human IgG1, IgG2, IgG3 or IgG4 Fc region. The
XX glycoprotein binds FcγmARIII with better affinity, or mediates antibody
XX dependent cell-mediated cytotoxicity more effectively, than the
XX glycoprotein including fucose. The antibody may be chimeric, humanised or
XX human and binds a B-cell surface marker, an ErbB receptor, a tumour-
XX associated antigen or an angiogenic factor, CD20, HER2, vascular
XX endothelial growth factor, CD40 or prostate stem cell antigen. The
XX composition is useful for treating cancer, autoimmune disease, an
XX inflammatory disorder or infection in a mammal
XX
XX Sequence 218 AA;
XX
XX Query Match 96.9%; Score 565; DB 6; Length 218;
XX Best Local Similarity 97.3%; Pred. No. 6.9e-49;
XX Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVGFNNYVVGVEVHNATK 60
XX DB 2 APEFLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVGFNNYVVGVEVHNATK 61
XX
XX QY 61 PREQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
XX DB 62 PREQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 111
XX
XX RESULT 12
XX ADD32013
XX ID ADD32013 standard; protein; 229 AA.
XX AC ADD32013;
XX DT 15-JAN-2004 (first entry)
XX DE Heterologous fusion protein related protein sequence SEQ ID NO:19.
XX KW heterologous fusion protein;
XX hyperglycosylated granulocyte-colony stimulating factor; G-CSF;
XX human albumin; human albumin analogue; immunoglobulin; Fc;
XX immunostimulant; protein therapy; neutrophil level;
XX insufficient circulating neutrophil level;
XX chronic congenital neutropenia.
XX OS Synthetic.
XX
XX WO2003076567-A2.
XX
XX 18-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US003120.
XX
XX 05-MAR-2002; 2002US-0361948P.
XX
XX (ELIL ) LILLY & CO ELI.

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PI Beals JM, Kuchibhotla U;  
 XX WPI; 2003-902770/82.  
 XX New heterologous fusion proteins with granulocyte-colony stimulating  
 PT factor activity, useful for increasing neutrophil levels and treating  
 PT patients with low circulating neutrophils, such as after chemotherapy or  
 PT in neutropenia.  
 XX  
 XX Disclosure; SEQ ID NO 19; 126pp; English.  
 XX  
 XX The present invention describes a heterologous fusion protein (I)  
 CC comprising a hyperglycosylated granulocyte-colony stimulating factor (G-  
 CC CSF) analogue fused to a polypeptide having human albumin, human albumin  
 CC analogues or fragments of human albumin, or the Fc portion of an  
 CC immunoglobulin, an analogue of the Fc portion of an immunoglobulin, or  
 CC fragments of the Fc portion of an immunoglobulin. Also described: (1) a  
 CC heterologous fusion protein, which is the product of the expression in a  
 CC host cell of an exogenous DNA sequence encoding (1); (2) an isolated  
 CC nucleic acid sequence comprising: (a) polynucleotides encoding (1); or  
 CC (b) a polynucleotide, which comprises any of 15 DNA sequences each  
 CC comprising 1044 base pairs (see ADD31996 to ADD32010), fused to the DNA  
 CC encoding a protein (i.e. human albumin, human albumin analogue or  
 CC fragments of human albumin); (3) increasing neutrophil levels in a mammal  
 CC comprising the administration of (1); (4) pharmaceutical formulations  
 CC adapted for the treatment of patients with insufficient neutrophil levels  
 CC comprising any of (1); (5) a vector comprising the polynucleotide of (2);  
 CC (6) host cells comprising the vector of (5), or expressing at least one  
 CC heterologous protein; and (7) producing (1). (1) has immunostimulant  
 CC activity, and can be used in protein therapy. (1) can be used for  
 CC increasing neutrophil levels in a mammal. (1) are particularly useful in  
 CC medicaments for the treatment of patients with insufficient circulating  
 CC neutrophil levels, or for the manufacture of a medicament for the  
 CC treatment of patients with insufficient circulating neutrophil levels.  
 CC The fusion protein is particularly useful for treating conditions  
 CC treatable by stimulation of circulating neutrophils, such as after  
 CC chemotherapy regimens or in chronic congenital neutropenia. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 XX Sequence 229 AA;  
 SQ

Query Match 96.9%; Score 565; DB 7; Length 229;  
 Best Local Similarity 97.3%; Pred. No. 7.3e-49;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDITLMSRTPEVTCVVDVVSQEDPEVQFNWYVDGVGVHNAKTK 60  
 DB 13 APELGGSPVFLPPPKDITLMSRTPEVTCVVDVVSQEDPEVQFNWYVDGVGVHNAKTK 72

QY 61 PREQFNSTYRWSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110  
 DB 73 PREQFNSTYRWSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 122

RESULT 13  
 AAE30927  
 ID AAE30927 standard; protein; 284 AA.  
 XX  
 XX AAE30927;  
 AC  
 XX  
 XX 24-FEB-2003 (first entry)  
 DT  
 XX  
 XX Gly8-Glu22-GLP-1-CEX-linker-Immunoglobulin G4 (IgG4) fusion protein.  
 DE  
 XX  
 XX Human; glucagon-like peptide 1; GLP-1; albumin; immunoglobulin; Ig;  
 KW therapy; non-insulin diabetes mellitus; obesity; antidiabetic; anorectic;  
 KW fusion protein.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Unidentified.  
 OS  
 XX Chimeric.  
 OS  
 XX WO200246227-A2.  
 FN

XX 13-JUN-2002.  
 PD  
 XX  
 XX 29-NOV-2001; 2001WO-US043165.  
 PF  
 XX  
 XX 07-DEC-2000; 2000US-0251954P.  
 PR  
 XX  
 XX (ELIL) LILLY & CO ELI.  
 PA  
 XX  
 XX Glaesner W, Micanovic R, Tschang SR;  
 PI WPI; 2003-018534/01.  
 XX  
 XX Novel heterologous fusion protein, useful for treating non-insulin  
 DR dependent diabetes mellitus or obesity, comprises a glucagon-like peptide  
 XX 1 compound fused to human albumin or to the Fc portion of an  
 PT immunoglobulin.  
 XX  
 XX Example 6; Page 83; 200pp; English.  
 PS  
 XX The invention relates to a heterologous fusion protein comprising a first  
 CC polypeptide fused to a second polypeptide, where the polypeptides has a N  
 CC terminus and a C-terminus and the first polypeptide is a glucagon-like  
 CC peptide 1 (GLP-1) compound and the second is a human albumin or its  
 CC analogue or fragment, or the Fc portion of an immunoglobulin (Ig) or its  
 CC analogue or fragment, where the C-terminus of first polypeptide is fused  
 CC to the N-terminus of the second polypeptide. The invention is useful for  
 CC normalising blood glucose levels in mammal, for treating a patient with  
 CC non-insulin diabetes mellitus or obesity, or for the manufacture of  
 CC medicament for treating the above mentioned diseases. The present  
 CC sequence is GLP-1 fusion protein  
 XX  
 XX Sequence 284 AA;  
 SQ

Query Match 96.9%; Score 565; DB 6; Length 284;  
 Best Local Similarity 97.3%; Pred. No. 9.5e-49;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDITLMSRTPEVTCVVDVVSQEDPEVQFNWYVDGVGVHNAKTK 60  
 DB 68 APELGGSPVFLPPPKDITLMSRTPEVTCVVDVVSQEDPEVQFNWYVDGVGVHNAKTK 127

QY 61 PREQFNSTYRWSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110  
 DB 128 PREQFNSTYRWSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 177

RESULT 14  
 AAM37346  
 ID AAM37346 standard; protein; 327 AA.  
 XX  
 XX AAM37346;  
 AC  
 XX  
 XX 11-MAY-1998 (first entry)  
 DT  
 XX  
 XX Immunoglobulin C-gamma-4 region.  
 DE  
 XX  
 XX Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;  
 KW gene amplification; immunotherapy; therapy; immunoglobulin; C-gamma-4;  
 KW constant region.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9741244-A1.  
 FN  
 XX  
 XX 06-NOV-1997.  
 PD  
 XX  
 XX 25-APR-1997; 97WO-US007039.  
 PF  
 XX  
 XX 01-MAY-1996; 96US-00644664.  
 PR  
 XX 06-DEC-1996; 96US-00761277.  
 PR  
 XX  
 XX (GENI-) GENITOPE CORP.  
 PA

XX Denney DW;  
 XX WPI; 1997-549743/50.  
 DR N-PSDB; AAT97189.  
 XX  
 XX Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at  
 PT least 2 different recombinant variable regions of immunoglobulin  
 PT molecules derived from B cell lymphoma cells.  
 XX  
 PS Example 10; Page 126-127; 177pp; English.  
 XX  
 CC This protein comprises an immunoglobulin (Ig) C-gamma-4 region. The  
 CC invention provides a method for the production of tumour-specific Ig  
 CC derived from a B-cell lymphoma patient. In the novel method, expression  
 CC plasmids containing the patient's VH region(s) joined to either a C-gamma  
 CC -3 (see AAT97188) or C-gamma-4 (see AAT97189) sequence and expression  
 CC plasmids containing the patient's VL region(s) joined to either a C-kappa  
 CC (see AAT97190) or C-lambda-2 (see AAT97191) sequence are cotransfected  
 CC along with a selectable and amplifiable marker into a cell line (e.g.  
 CC BMS147.G1.4), and transfected cells are then subjected to selection and  
 CC amplification. The method permits the production of a multivalent vaccine  
 CC which reflects the degree of somatic variation found within the patient's  
 CC tumour. These novel multivalent vaccines provide superior vaccines for  
 CC the treatment of B-cell lymphoma  
 XX  
 SQ Sequence 327 AA;  
 Query Match 96.9%; Score 565; DB 2; Length 327;  
 Best Local Similarity 97.3%; Pred. No. 1.1e-48;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 DB 111 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170  
 QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 171 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 220

RESULT 15  
 AAM47859  
 ID AAM47859 standard; protein; 327 AA.  
 XX  
 AC AAM47859;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Human Ig-G4 heavy chain constant region amino acid sequence.  
 XX  
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
 KW transgenic plant.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WC200183529-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 28-APR-2001; 2001NO-US013932.  
 XX  
 PR 28-APR-2000; 2000US-0200298P.  
 XX  
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.  
 XX  
 PI Larrick JW, Wycoff KL;  
 XX  
 PI WPI; 2002-041481/05.  
 DR N-PSDB; ABA05288.  
 XX  
 PT Immunoadhesin for treating human rhinovirus infection comprises chimeric

PT intercellular adhesion molecule-1, and optionally a J chain and secretory  
 XX component in association.  
 XX Disclosure; Fig 7; 138pp; English.  
 XX  
 CC The invention relates to an immunoadhesin comprising: (a) a chimeric  
 CC intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor  
 CC protein linked to at least a portion of an immunoglobulin heavy chain;  
 CC and (b) optionally a J chain and secretory component associated with the  
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific  
 CC glycosylation and virucide activity. The immunoadhesin is useful for  
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or  
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and  
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding  
 CC sites, interfering with virus entry or uncoating and directing premature  
 CC release of viral RNA and formation of empty capsids. Expression of the  
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.  
 CC Immunoadhesin having multiple binding sites have a higher effective  
 CC affinity for the virus, thereby increasing the effectiveness of the  
 CC immunoadhesin. Association of secretory component and immunoglobulin J  
 CC chain increases the stability of the immunoadhesin in the mucosal  
 CC environment. Production is significantly less expensive in plants than in  
 CC animal cell culture and production in plants is safer for human use,  
 CC since plants are not known to harbor any animal viruses. The present  
 CC sequence is that of a human immunoglobulin protein sequence, useful to  
 XX the invention  
 SQ Sequence 327 AA;

Search completed: April 29, 2004, 08:44:23  
 Job time : 52.5 secs



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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:12 ; Search time 50.5 Seconds  
(without alignments)

615.450 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLFPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	98.1	110	3	AAY54998
2	570.5	97.2	109	3	AAY54996 Mutated C
3	562	95.7	468	2	Aaw85689 D9D10 hea
4	562	95.7	488	3	AAY97175 Human FGF
5	562	95.7	497	3	AAY97174 Human FGF
6	562	95.7	525	3	AAY97173 Human FGF
7	562	95.7	711	2	Aaw85692 Motabii f
8	561	95.6	447	6	Aae33524 Human AQC
9	560	95.4	251	6	Aae35231 Human imm
10	558	95.1	232	5	Abb1492 Human mut
11	558	95.1	232	5	Abb1491 Human mut
12	558	95.1	250	6	Aae35220 Human mod
13	558	95.1	251	2	AAY05688 Modified
14	558	95.1	251	2	Aaw97756 Modified
15	558	95.1	251	3	AAB07541 Amino aci
16	558	95.1	251	6	Aae35218 Human mod
17	558	95.1	251	6	Aae35219 Human imm
18	558	95.1	328	5	Abb1493 Ztnfr12-t
19	558	95.1	332	6	Aae35228 Human TAC
20	558	95.1	344	6	Aae35224 Human TAC
21	558	95.1	348	6	Aae35225 Human TAC
22	558	95.1	357	6	Aae35226 Human TAC
23	558	95.1	392	6	Aae35223 Human TAC
24	558	95.1	473	5	Abb1645 Zcytor19
25	558	95.1	476	5	Aau76912 Human CRF

26	558	95.1	476	6	Aae30845	Human CRP
27	558	95.1	484	5	Aau76916	Human zcy
28	558	95.1	484	6	Aae30844	Human zcy
29	558	95.1	556	5	Aae29073	Human IL-
30	558	95.1	559	4	AAB85286	IL-20RA-1
31	558	95.1	559	5	ABG67217	IL-20RA e
32	558	95.1	559	5	Aae23361	Human IL-
33	558	95.1	573	5	Aae29072	Human IL-
34	558	95.1	594	4	AAB85274	Human IL-
35	558	95.1	594	4	Aau04062	Human IL-
36	558	95.1	594	5	ABG67205	IL-20RA e
37	558	95.1	594	5	Aae23358	Human IL-
38	558	95.1	764	5	ABD05743	Human zcy
39	558	95.1	764	7	ADD68180	Human zcy
40	557	94.9	110	2	AAR27680	Human imm
41	557	94.9	116	2	AAR41684	Human imm
42	557	94.9	116	2	AY42621	Human IGG
43	557	94.9	212	2	AAR87023	Human IGG
44	557	94.9	212	2	Aaw02305	Human IGG
45	557	94.9	212	2	AAR97264	Human imm

## ALIGNMENTS

### RESULT 1

AAY54998  
ID AAY54998 standard; protein; 110 AA.

XX

XX AAY54998;

XX 17-FEB-2000 (first entry)

DT

XX

DE Mutated CH2 sequence Gldeltaac.

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Binding molecule; CH2 sequence; complement dependent lysis; Fc gammaRIIb;  
cell-mediated destruction; human; immunoglobulin G; Igg heavy chain;  
B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
Crohn's disease; graft-vs-host disease; organ transplant rejection;  
bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
allimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
sickle cell anaemia; coronary artery occlusion.

Synthetic.

WO9958572-A1.

18-NOV-1999.

07-MAY-1999; 99WO-CB001441.

08-MAY-1998; 98GB-00009951.

{UYCA-} UNIV CAMBRIDGE TECH SERVICES LTD.

Armour KL, Clark MR, Williamson LM;

WPI; 2000-039075/03.

Immunoglobulin-derived binding molecules that do not activate complement

or trigger cytotoxic activities and maintaining desirable immunoglobulin

properties.

Claim 12; Fig 17; 81pp; English.

This sequence represents the mutated CH2 molecule Gldeltaac, and is a

binding molecule of the invention. The recombinant binding molecule is

capable of binding a target molecule without triggering complement

dependent lysis, or the cell-mediated destruction of the target

comprises: (a) a binding domain capable of binding a target molecule; and

(b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
 CC molecule is used to bind a target molecule (especially FcγγmαRIIb  
 CC causing inhibition of B cell activation, mast cell degranulation or  
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
 CC binding of a second binding molecule, e.g. an antibody, to the target  
 CC molecule. The binding molecule is useful for the treatment of graft-vs-  
 CC host disease, organ transplant rejection, bone-marrow transplant  
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
 CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
 CC coronary artery occlusion). The binding molecules do not activate  
 CC complement or trigger cytotoxic activities through FcγγmαRIIb and desirable  
 CC IgG properties have been retained. The polypeptides do not contain non-  
 CC human amino acids, and are therefore likely to have reduced  
 CC immunogenicity. Further, they still bind Protein A, which is consistent  
 CC with being able to cross the human placenta through interaction with FcRn  
 CC (neonatal Fc receptor)  
 XX  
 XX Sequence 110 AA;

Query Match 98.1%; Score 576; DB 3; Length 110;  
 Best Local Similarity 99.1%; Pred. No. 9.3e-52;  
 Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 DB 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 QY 61 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVKNKGLPSSIEKTIKAK 110  
 DB 61 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVKNKGLPSSIEKTIKAK 110

RESULT 2  
 AAY54996  
 ID AAY54996 standard; protein; 109 AA.

XX AAY54996;

DT 17-FEB-2000 (first entry)

DE Mutated CH2 sequence Gldeltaab.

XX Binding molecule; CH2 sequence; complement dependent lysis; FcγγmαRIIb;  
 KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
 KW bone-marrow transplant rejection; autoimmunity disease; asthma; allergy;  
 KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
 KW sickle cell anaemia; coronary artery occlusion.

XX Synthetic.

XX WO9558572-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001441.

XX 08-MAY-1998; 98GB-00009951.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Armour KL, Clark MR, Williamson LM;

XX WPI; 2000-039075/03.

XX Immunoglobulin-derived binding molecules that do not activate complement  
 PT or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.

PS Claim 12; Fig 17; 8lpp; English.

XX This sequence represents the mutated CH2 molecule Gldeltaab, and is a  
 CC binding molecule of the invention. The recombinant binding molecule is  
 CC capable of binding a target molecule without triggering complement  
 CC dependent lysis, or the cell-mediated destruction of the target  
 CC comprises: (a) a binding domain capable of binding a target molecule; and  
 CC (b) an effector domain that is homologous to all or part of a constant  
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
 CC molecule is used to bind a target molecule (especially FcγγmαRIIb  
 CC causing inhibition of B cell activation, mast cell degranulation or  
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
 CC binding of a second binding molecule, e.g. an antibody, to the target  
 CC molecule. The binding molecule is useful for the treatment of graft-vs-  
 CC host disease, organ transplant rejection, bone-marrow transplant  
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
 CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
 CC coronary artery occlusion). The binding molecules do not activate  
 CC complement or trigger cytotoxic activities through FcγγmαRIIb and desirable  
 CC IgG properties have been retained. The polypeptides do not contain non-  
 CC human amino acids, and are therefore likely to have reduced  
 CC immunogenicity. Further, they still bind Protein A, which is consistent  
 CC with being able to cross the human placenta through interaction with FcRn  
 CC (neonatal Fc receptor)  
 XX

SQ Sequence 109 AA;

Query Match 97.2%; Score 570.5; DB 3; Length 109;

Best Local Similarity 99.1%; Pred. No. 3.4e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60

DB 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 59

QY 61 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVKNKGLPSSIEKTIKAK 110

DB 60 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVKNKGLPSSIEKTIKAK 109

RESULT 3

AAY85689

ID AAY85689 standard; protein; 468 AA.

XX AAY85689;

DT 12-AUG-1999 (first entry)

DE D9D10 heavy chain fusion protein.

XX Antibody; humanised; variable region; heavy chain; light chain;

KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;

KW immune disease; multiple sclerosis; Crohn's disease; skin disorders;

KW inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;

KW multivalent; ruminant.

XX Synthetic.

OS Mus musculus.

XX Location/Qualifiers

PH Key 1...20 "D9D10 light chain signal peptide"

FT Peptide /note= "D9D10 light chain signal peptide"

FT Domain 21..137

FT Domain /note= "Humanised heavy chain variable domain of D9D10"

FT Domain 138..467

FT Domain /note= "Human IgG1 heavy chain constant domain"

FT Misc-difference 468

FT /note= "Leu added by cloning strategy"



CC mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung,  
 CC rectal, testis and cervical tumors), neovascularization (e.g. diabetic  
 CC retinopathy, neovascular glaucoma, wound healing and corneal scarring)  
 CC and hyper-proliferation of vascular smooth muscle cells (e.g.  
 CC postangioplasty and postatherectomy restenosis)  
 XX Sequence 438 AA;  
 SQ

Query Match 95.7%; Score 562; DB 3; Length 488;  
 Best Local Similarity 95.5%; Pred. No. 1.6e-49;  
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSVFLPPPKKDTLMSRPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 DB 272 APELEGGSVFLPPPKKDTLMSRPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 331  
 QY 61 PREEQNSTYRVSVLTVLHQDLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 332 PREEQNSTYRVSVLTVLHQDLNGKEYKCKVSNKGLPSSIEKTIISKAK 381

RESULT 5  
 ID AAY97174 standard; protein; 497 AA.  
 AC AAY97174;  
 DT 04-DEC-2000 (first entry)  
 XX Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.  
 DE FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;  
 KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;  
 KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;  
 KW ophthalmological; anti-proliferative.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..21 /label= FGF-R1\_signal\_peptide  
 FT Domain 22..257 /label= FGF-R1\_extracellular\_domain  
 FT /note= "The Ig I segment and acid box are deleted"  
 FT Domain 59..111 /label= Ig\_II\_segment  
 FT Domain 157..222 /label= Ig\_III\_segment  
 FT Peptide 258..265 /label= Linker  
 FT Region 266..497 /label= Human IgG1\_Fc\_region  
 FT /note= "Contains hinge region and domains CH2 and CH3"  
 FT Misc-difference 285 /label= L285B  
 FT /note= "This mutation decreases the affinity of the Fc  
 FT portion for Fc receptors"  
 FT Misc-difference 385 /label= P385S  
 FT /note= "This mutation decreases the affinity of the Fc  
 FT portion for complement"  
 XX W0200046380-A2.  
 XX 10-AUG-2000.  
 XX 07-FEB-2000; 2000WO-US003166.  
 XX 08-FEB-1999; 99US-0119002P.  
 XX (CHIR ) CHIRON CORP.  
 XX Kavanaugh WM, Ballinger M;  
 PI

XX WPI, 2000-514961/46.  
 DR N-FSDB; AAA52131.  
 XX New polypeptide comprising a fibroblast growth factor receptor  
 FT extracellular domain fused to a heterologous oligomerization domain for  
 FT treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.  
 XX Claim 14; Page 65-66; 70pp; English.  
 PS Novel fusion protein constructs comprise a fibroblast growth factor (FGF)  
 XX receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin  
 CC (Ig) I segment fused to a heterologous oligomerization domain that  
 CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4  
 CC region, or light chain of an immunoglobulin molecule, or a peptide with a  
 CC leucine zipper motif. The Ig I segment is not necessary for binding of  
 CC acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the  
 CC affinity for aFGF and heparin, protects the core of the molecule from  
 CC proteolysis, and abrogates the heparin requirement for aFGF binding. The  
 CC new fusion polypeptides are better FGF inhibitors than FGF-R monomer  
 CC proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at  
 CC subnanomolar concentrations and were 20-fold more potent than the FGF-R  
 CC monomer protein as competitors of bFGF binding to immobilized FGF-R. The  
 CC fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-  
 CC mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung,  
 CC rectal, testis and cervical tumors), neovascularization (e.g. diabetic  
 CC retinopathy, neovascular glaucoma, wound healing and corneal scarring)  
 CC and hyper-proliferation of vascular smooth muscle cells (e.g.  
 CC postangioplasty and postatherectomy restenosis)  
 XX Sequence 497 AA;  
 SQ

Query Match 95.7%; Score 562; DB 3; Length 497;  
 Best Local Similarity 95.5%; Pred. No. 1.6e-49;  
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSVFLPPPKKDTLMSRPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 DB 281 APELEGGSVFLPPPKKDTLMSRPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 340  
 QY 61 PREEQNSTYRVSVLTVLHQDLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 341 PREEQNSTYRVSVLTVLHQDLNGKEYKCKVSNKGLPSSIEKTIISKAK 390

RESULT 6  
 ID AAY97173 standard; protein; 525 AA.  
 AC AAY97173;  
 DT 04-DEC-2000 (first entry)  
 XX Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.  
 DE FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;  
 KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;  
 KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;  
 KW ophthalmological; anti-proliferative.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..21 /label= FGF-R1\_signal\_peptide  
 FT Domain 22..285 /label= FGF-R1\_extracellular\_domain  
 FT /note= "Ig I segment is deleted"  
 FT Domain 37..44 /label= Acid\_box\_segment  
 FT Domain 87..139 /label= Ig\_II\_segment  
 FT Peptide 286..293

```

FT      Region      /label= Linker
FT      294. .525
FT      /label= Human IgG1 Fc region
FT      /note= "Contains hinge region and domains CH2 and CH3"
FT      Misc-difference 313
FT      /label= L313E
FT      /note= "The mutation decreases the affinity of the Fc
FT      portion for Fc receptors"
FT      Misc-difference 409
FT      /label= P409S
FT      /note= "The mutation decreases the affinity of the Fc
FT      portion for complement"
FT      445. .250
FT      /label= Ig_III_segment
FT      XX
FT      WO200046380-A2.
FT      XX
FT      10-AUG-2000.
FT      XX
FT      07-FEB-2000; 2000WO-US003166.
FT      XX
FT      08-FEB-1999; 99US-0119002P.
FT      XX
FT      (CHIR ) CHIRON CORP.
FT      XX
FT      Kavanaugh WW, Ballinger M;
FT      XX
FT      WPI: 2000-514961/46.
FT      XX
FT      N-PSDB; AA52130.
FT      XX
FT      New polypeptide comprising a fibroblast growth factor receptor
FT      extracellular domain fused to a heterologous oligomerization domain for
FT      treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
FT      XX
FT      Claim 14; Page 61-62; 70pp; English.
FT      XX
FT      Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
FT      receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
FT      (Ig) I segment fused to a heterologous oligomerization domain that
FT      comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
FT      region, or light chain of an immunoglobulin molecule, or a peptide with a
FT      leucine zipper motif. The Ig I segment is not necessary for binding of
FT      acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
FT      affinity for aFGF and heparin, protects the core of the molecule from
FT      proteolysis, and abrogates the heparin requirement for aFGF binding. The
FT      new fusion polypeptides are better FGF inhibitors than FGF-R monomer
FT      proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at
FT      subnanomolar concentrations and were 20-fold more potent than the FGF-R
FT      monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
FT      fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
FT      mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung,
FT      rectal, testis and cervical tumours), neovascularization (e.g. diabetic
FT      retinopathy, neovascular glaucoma, wound healing and corneal scarring)
FT      and hyper-proliferation of vascular smooth muscle cells (e.g.
FT      postangioplasty and postatherectomy restenosis)
FT      XX
FT      Query Match      95.7%; Score 562; DB 3; Length 525;
FT      Best Local Similarity 95.5%; Pred. No. 1.8e-49;
FT      Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
FT      XX
QY      1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB      309 APELEGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368
QY      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB      369 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 418
FT      XX
FT      RESULT 7
FT      AAW85692

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ID      XX      AAW85692 standard; protein; 711 AA.
AC      AAW85692;
DT      12-AUG-1999 (first entry)
DE      MoTabII fusion protein.
XX      XX
XX      Antibody; humanised; variable region; heavy chain; light chain;
XX      interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
XX      immune disease; multiple sclerosis; Crohn's disease; skin disorders;
XX      inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
XX      multivalent; ruminant.
XX      Synthetic.
XX      XX
FH      Key      Location/Qualifiers
FT      Peptide 1..20
FT      /label= Mouse_D9D10_light_chain_signal_peptide
FT      Domain 21..137
FT      /note= "Humanised heavy chain variable domain of D9D10"
FT      Domain 138..467
FT      /note= "Human IgG1 heavy chain constant domain"
FT      Misc-difference 468
FT      /note= "Leu added by cloning strategy"
FT      Region 469..472
FT      /label= Gly(3)Ser_linker
FT      Domain 473..711
FT      /label= Humanised_D9D10_ScFv
XX      XX
XX      WO9909055-A2.
XX      XX
XX      25-FEB-1999.
XX      XX
XX      14-AUG-1998; 98WO-EP005165.
XX      XX
XX      18-AUG-1997; 97EP-00870122.
XX      18-JUN-1998; 98EP-00870139.
XX      (INNO-) INNOGENETICS NV.
XX      Buyse M, Sablon E;
XX      WPI: 1999-180969/15.
XX      N-PSDB; AAW85692.
XX      XX
XX      New engineered antibodies which bind and neutralise interferon-gamma -
XX      useful for prevention and treatment of septic shock, cachexia, immune
XX      diseases and skin disorders.
XX      Disclosure; Fig 20; 134pp; English.
XX      XX
XX      New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
XX      be used as a medicant, for preventing or treating septic shock, cachexia,
XX      immune diseases including multiple sclerosis and Crohn's disease and skin
XX      disorders including bullous, inflammatory and neoplastic dermatoses. The
XX      antibody is selected from a single chain antibody (scFv), a chimeric
XX      antibody or diabody comprising the humanised variable domain of the
XX      monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody;
XX      or a ruminant antibody. The antibodies are also useful for determining
XX      IFN gamma levels in a sample
XX      XX
XX      Sequence 711 AA;
XX      Query Match      95.7%; Score 562; DB 2; Length 711;
XX      Best Local Similarity 95.5%; Pred. No. 2.5e-49;
XX      Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY      1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB      251 APELEGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
QY      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

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Db 311 PREEOYNSTYRVSVLTVLHODWLNKGYCKVSNKALPASIEKTSKAK 360  
|||||

RESULT 8  
ID AAE33524  
XX AAE33524 standard; protein; 447 AA.  
XX AAE33524;  
DT 02-APR-2003 (first entry)  
DE Human AQC2 heavy chain mutant protein, hsaQC2.  
XX  
XX Human; very late activation antigen; VLA-1; beta1 containing integrin;  
XX immunological disorder; inflammatory disorder; skin related condition;  
XX psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
XX fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;  
XX fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
XX irritable bowel syndrome; colitis; colorectal cancer; vascular disease;  
XX atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;  
XX gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
XX osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
XX systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
XX renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
XX hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
XX graft versus host disease; myocardial ischaemia; mutant; mutin.  
XX  
OS Homo sapiens.  
XX  
PN WO200283854-A2.  
XX  
PD 24-OCT-2002.  
XX  
XX  
PF 12-APR-2002; 2002WO-US011521.  
XX  
PR 13-APR-2001; 2001US-0283794P.  
PR 06-JUL-2001; 2001US-0303689P.  
XX  
XX (BIOJ) BIOGEN INC.  
XX  
XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
XX WPI; 2003-093009/08.  
XX  
XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
XX mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
XX burns, dermatitis, and abnormal proliferation of hair follicle cells or  
XX fibrosis.  
XX  
XX Example 23; Page 92; 2489p; English.

XX  
XX The present invention relates to novel antibodies that specifically bind  
XX to very late activation (VLA-1; beta1 containing integrins) antigens and  
XX methods of using these antibodies to treat immunological disorders. The  
XX anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
XX mediated immunological or inflammatory disorders such as skin related  
XX conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
XX proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
XX fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
XX bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
XX intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
XX gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
XX vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
XX periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
XX autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
XX arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
XX failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
XX polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
XX immediate hypersensitivity), graft and transplant rejections, graft  
XX versus host disease, conjunctivitis, swelling occurring after injury,  
XX myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
XX human AQC2 heavy chain mutant protein, hsaQC2

XX Sequence 447 AA;  
Query Match 95.6%; Score 561; DB 6; Length 447;  
Best Local Similarity 95.5%; Pred. No. 1.8e-49;  
Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 232 APEAAGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 291  
QY 61 PREEOYNSTYRVSVLTVLHODWLNKGYCKVSNKALPASIEKTSKAK 110  
DB 292 PREEOYNSTYRVSVLTVLHODWLNKGYCKVSNKALPASIEKTSKAK 341  
RESULT 9  
ID AAE35231 standard; protein; 251 AA.  
XX AAE35231;  
XX AAE35231;  
DT 28-MAY-2003 (first entry)  
DE Human immunoglobulin gamma1 mutant protein, A134S.  
XX  
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
XX TAC1; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
XX anaemia; gene therapy; cytostatic; anti-inflammatory; immunosuppressive;  
XX glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
XX dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
XX autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
XX diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;  
XX mutant; mutin.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Binding-site 38..41 /note= "FcgammaRI binding site"  
FT Misc-difference 134 /note= "Wild-type Ala is replaced with Ser"  
XX  
XX WO200294852-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 20-MAY-2002; 2002WO-US015910.  
XX  
XX 24-MAY-2001; 2001US-0293343P.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX Rixon MW, Gross JA;  
XX WPI; 2003-148455/14.  
XX  
XX Transmembrane activator and calcium modulator and cyclophilin ligand-  
XX interactor (TAC1)-immunoglobulin fusion protein, for treating cancer or  
XX diabetes, comprises a TAC1 receptor group and an immunoglobulin group.  
XX  
XX Example 1; Col; 71pp; English.  
XX  
XX The invention relates to fusion proteins comprising transmembrane  
XX activator and calcium modulator and cyclophilin ligand-interactor (TAC1)  
XX receptor group that binds tumour necrosis factor-like protein (ZTNF) 2 or  
XX ZTNF4; and an immunoglobulin group comprising a constant region of an  
XX immunoglobulin. The invention is used to manufacture a medicament for  
XX inhibiting the proliferation of tumour cells in a mammalian subject. The  
XX composition comprising the fusion protein may also be used in treating  
XX autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
XX sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal

CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
CC rejection, anaemia and septic shock. The fusion proteins are also used in  
CC gene therapy. The present sequence is human immunoglobulin gamma1 mutant  
CC protein. This sequence is used in the exemplification of the invention.  
CC Note: This sequence is not shown in the specification, however it is  
CC constructed based on human immunoglobulin gamma1 protein (SEQ ID NO:6)  
CC sequence shown in column 92-93 (AAE35214)  
XX  
SQ Sequence 251 AA;

designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antithrombotic, antiasthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. Human Ztnfr12 is located to chromosome 22q13.2. The present sequence represents a mutated Fc protein designated Fc5, which is used in an example from the present invention

XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Gross JA, Xu W, Henne RM, Grant FJ;  
 XX DR WPI; 2002-508212/54.  
 XX DR N-PSDB; AEN89444.  
 XX PT Novel isolated human tumor necrosis factor receptor polypeptide, termed  
 XX PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
 XX PT renal failure or renal disease and lymphoma.  
 XX PS Example 4; Page 146; 154pp; English.  
 XX CC The present invention describes a human tumor necrosis factor receptor  
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive  
 CC activities, and can be used in gene therapy. (I) can be used for  
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12  
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B  
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for  
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating  
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia  
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,  
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure  
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid  
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal  
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or  
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host  
 CC disease, graft rejection and Crohn's disease. (I) is useful for  
 CC modulating the immune system, for regulating B cell responses and  
 CC development, for modulating development of other cells, antibody  
 CC production and cytokine production, and for modulating T and B cell  
 CC communication. Human Ztnfr12 is located to chromosome 22q13.2. The  
 CC present sequence represents a mutated Fc protein designated Fc4, which is  
 CC used in an example from the present invention  
 XX SQ Sequence 232 AA;  
 Query Match 95.1%; Score 558; DB 5; Length 232;  
 Best Local Similarity 95.5%; Pred. No. 1.7e-49;  
 Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 60  
 DB 16 APEAGAPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 75  
 QY 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTISKAK 110  
 DB 76 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTISKAK 125  
 RESULT 12  
 AA35220  
 ID AAB35220 standard; protein; 250 AA.  
 XX AC AAB35220;  
 XX AC AAB35220;  
 XX DT 28-MAY-2003 (first entry)  
 XX DE Human modified immunoglobulin moiety #3.  
 XX KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;  
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.  
 XX OS Homo sapiens.  
 OS Synthetic.

XX PN WO200294852-A2.  
 XX PD 28-NOV-2002.  
 XX PP 20-MAY-2002; 2002WO-US015910.  
 XX PR 24-MAY-2001; 2001US-0293343P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Rixon MW, Gross JA;  
 XX DR WPI; 2003-148455/14.  
 XX DR N-PSDB; AAD53758.  
 XX CC Transmembrane activator and calcium modulator and cyclophilin ligand-  
 CC interactor (TACI)-immunoglobulin fusion protein, for treating cancer or  
 CC diabetes, comprises a TACI receptor group and an immunoglobulin group.  
 XX PS Disclosure; Col 110-111; 71pp; English.  
 XX CC The invention relates to fusion proteins comprising transmembrane  
 CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)  
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF) 2 or  
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an  
 CC immunoglobulin. The invention is used to manufacture a medicament for  
 CC inhibiting the proliferation of tumour cells in a mammalian subject. The  
 CC composition comprising the fusion protein may also be used in treating  
 CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
 CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal  
 CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
 CC rejection, anaemia and septic shock. The fusion proteins are also used in  
 CC gene therapy. The present sequence is human modified immunoglobulin  
 XX SQ Sequence 250 AA;  
 Query Match 95.1%; Score 558; DB 6; Length 250;  
 Best Local Similarity 95.5%; Pred. No. 1.8e-49;  
 Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 60  
 DB 35 APEAGAPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 94  
 QY 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTISKAK 110  
 DB 95 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTISKAK 144  
 RESULT 13  
 AA05688  
 ID AA05688 standard; protein; 251 AA.  
 XX AC AA05688;  
 XX AC AA05688;  
 XX DT 19-JUL-1999 (first entry)  
 XX DE Modified human IgG Fc sequence.  
 XX KW ZTNFR-6; tumour necrosis factor receptor-6; human; IgG1; Fc region;  
 KW cell maturation; bone cell regulation; mutant.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 38 /note= "Leu in native sequence"  
 FT Misc-difference 39 /note= "Leu in native sequence"  
 FT Misc-difference 41





Search completed: April 29, 2004, 08:44:21  
Job time : 51.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:33 ; Search time 13.5 Seconds

(without alignments)  
783.783 Million cell updates/sec

Title: US-09-674-857-3  
Perfect score: 587  
Sequence: 1 APPVAGGSVLFPPPKPDKT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	557	94.9	234	2 PT0207	Ig gamma chain C r
2	557	94.9	255	4 S31866	Ig gamma-1 chain C
3	557	94.9	330	1 GHU	Ig gamma-1 chain C
4	537	94.3	274	2 S69339	Ig heavy chain v r
5	533	94.2	327	1 G4HU	Ig gamma-4 chain C
6	543.5	92.6	326	1 G2HU	Ig gamma-2 chain C
7	539	91.8	377	2 A60764	Ig gamma-3 chain C
8	539	91.8	377	2 A23511	Ig gamma-3 chain C
9	519	88.4	289	1 G3HUI	Ig gamma-3 heavy c
10	458	78.0	328	2 I47159	Ig gamma-2b chain
11	458	78.0	328	2 I47160	Ig gamma 2a chain
12	453	77.2	277	2 I47162	Ig gamma 4 chain c
13	440	75.0	470	2 S22080	Ig heavy chain pre
14	434	73.9	328	2 I47161	Ig gamma 3 chain c
15	434	73.9	328	2 I47158	Ig gamma 1 chain c
16	431	73.4	333	2 PS0018	Ig gamma-2b chain
17	421	71.7	308	2 S30554	Ig heavy chain C r
18	421	71.7	323	1 GHRB	Ig gamma chain C r
19	421	71.7	329	1 G2GP	Ig gamma-2 chain C
20	421	71.7	472	2 S31459	Ig gamma-1 chain
21	418	71.2	329	1 G3MSC	Ig gamma-3 chain C
22	418	71.2	398	1 G3MSM	Ig gamma-3 chain C
23	410	69.8	377	2 S06611	Ig gamma-2 chain C
24	397	67.6	405	1 G2MSBM	Ig gamma-2b chain
25	397	67.6	474	1 G2MS11	Ig gamma-2b chain
26	396	67.5	324	1 G1MS	Ig gamma-1 chain C
27	396	67.5	329	2 S00847	Ig gamma-2c chain C
28	396	67.5	393	1 G1MSM	Ig gamma-1 chain C
29	396	67.5	444	2 PC4436	monoclonal antibody

ALIGNMENTS

RESULT 1

PT0207  
Ig gamma chain C region - chimpanzee  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C:Accession: PT0207  
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A:Title: Nucleotide sequence of chimpanzee Ec and hinge regions.  
A:Reference number: PT0207; MUID:91287716; PMID:2062315  
A:Accession: PT0207  
A:Molecule type: mRNA  
A:Residues: 1-234 <EHR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 557; DB 2; Length 234;  
Best Local Similarity 94.5%; Pred. No. 3.6e-48;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY	1	APPVAGGSVLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB	25	APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 84
QY	61	PREEQYNSTYRVSVLTIVLHQLDLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB	85	PREEQYNSTYRVSVLTIVLHQLDLNGKEYCKVSNKGLPSSIEKTSKAK 134

RESULT 2

S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filipula, D.  
Submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:G33068; PIDM:CAA49866.1; PID:G33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 94.9%; Score 557; DB 4; Length 255;  
Best Local Similarity 94.5%; Pred. No. 4e-48;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

A;Accession: A91723  
A:Molecule type: Protein  
A:Residues: 1-96,'R','98-197','D','199-238','E','240','M','242-266','D','268-271','D','273-330 <Scalpa  
A>Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A:Reference number: A95565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R;Draker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A>Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunologic  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C;Genetics:  
A;Gene: IGHG1  
A;Cross-references: GDB:I20085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
C;Introns: 99/1; 114/1; 224/1  
C;Context: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 94.9%; Score 557; DB 1; Length 330;  
Best Local Similarity 94.5%; Pred. No. 5.4e-48;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAATK 60  
Db 114 APBLGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAATK 173

Qy 61 PREEQYNSTYRVVSVLTFLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110  
Db 174 PREEQYNSTYRVVSVLTFLHQDWLNGKEYKCKVSNKALPAPIETISKAK 223

RESULT 4  
S69339  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C;Accession: S69339; S72664  
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A;Accession: S69339  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A;Cross-references: EMBL:X81695  
R;Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A;Accession: S72664  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140,'C','142-374 <KH2>  
A;Cross-references: EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 94.9%; Score 557; DB 2; Length 374;  
Best Local Similarity 94.5%; Pred. No. 6.2e-48;

G2HU  
IG gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain  
A;Reference number: A93906; MUID:82197621; PMID:6804948

Qy	1	APPVAGGSVFLFP	PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV	DGVGEVHNAKTK	60
	111	A	PPVA-GFSVFLFP	PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV	DGVGEVHNAKTK
Db					
Qy	61	PREEQNSTYRV	VSVLTVLHQDWLNGKEYCKVKNKGLPSIIETISKAK	110	

Db 170 PREEQNSTFRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTK 219

RESULT 7

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert

A:Reference number: A60764; MUID:90007613; PMID:2571587

A:Accession: A60764

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 539; DB 2; Length 377;

Best Local Similarity 90.9%; Pred.No. 3.9e-46; Indels 0; Gaps 0;

Matches 100; Conservative 4; Mismatches 6;

Qy 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 161 APPELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 220

Qy 61 PREEOYNSTRVSVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110

Db 221 PREEQNSTFRVSVLTVLHODWLNKGYKCKVSNKGLPAPIEKTISKTK 270

RESULT 8

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co

A:Reference number: A23511; MUID:86148507; PMID:3081877

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

A:Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056

C:Genetics:

A:Gene: IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.3%; Score 539; DB 2; Length 377;

Best Local Similarity 90.3%; Pred.No. 3.9e-46; Indels 0; Gaps 0;

Matches 100; Conservative 4; Mismatches 6;

Qy 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 161 APPELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 220

Qy 61 PREEOYNSTRVSVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110

Db 221 PREEQNSTFRVSVLTVLHODWLNKGYKCKVSNKGLPAPIEKTISKTK 270

RESULT 9

G3HUI

Ig gamma-3 heavy chain disease proteins - human

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999

C:Accession: A90442; A92219; A90198; A93915; A02149

R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy

A:Reference number: A90442; MUID:81021548; PMID:6774747

A:Contents: heavy chain disease protein Wis

A:Accession: A90442

A:Molecule type: protein

A:Residues: 1-289 <FRA>

A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchai

A:Note: this protein lacks most of the V' region and all of the CH1 region. Residue 12 c

A:Note: the sequence of residues 42-76 was taken from the reference that follows

R:Michaelson, I.B.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat

A:Reference number: A92219; MUID:77118561; PMID:402363

A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein

A:Accession: A92219

A:Molecule type: protein

A:Residues: 12-97 <MIC>

A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamm

A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte

R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.

Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the

A:Reference number: A90198; MUID:77021516; PMID:823945

A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues

A:Accession: A90198

A:Molecule type: protein

A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>

A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the

R:Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982

A:Title: Gamma heavy chain disease in man: cDNA sequence supports partial gene deletion

A:Reference number: A93915; MUID:82247835; PMID:6808505

A:Contents: heavy chain disease protein Om

A:Accession: A93915

A:Molecule type: mRNA

A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-15

A:Note: a carboxyl-terminal lys is removed posttranslationally

A:Note: this sequence may represent an allelic form or another gamma chain subclass

C:Comment: The heavy chain disease protein Wis is shown.

C:Genetics:

A:Gene: GDB:IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglytamic acid

F;203-270/Domain: immunoglobulin homology <IMM>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 88.4%; Score 519; DB 1; Length 289;

Best Local Similarity 86.4%; Pred.No. 2.8e-44; Indels 0; Gaps 0;

Matches 95; Conservative 9; Mismatches 6;

Qy 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 74 APPELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 133

Qy 61 PREEOYNSTRVSVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110

Db 134 PREEQNSTFRVSVLTVLHODWLNKGYKCKVSNKGLPAPIEKTISKTK 183

RESULT 10

I47160

Ig gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47160  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126  
C:Genetics:  
A:Gene: IgG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 78.0%; Score 458; DB 2; Length 328;  
Best Local Similarity 78.8%; Pred. No. 4.1e-38;  
Matches 82; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
QY 7 GPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKPREQY 66  
DB 116 GPSVFIFPPPKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKPREQY 175  
QY 67 NSTYRVSVLTVLHQDLNGLKEPKYCKVSNKGLPSSIEKTIISKAK 110  
DB 176 NSTYRVSVLPIQHODWLNGLKEPKYCKVSNKGLPAPITRIISKAK 219  
RESULT 11  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124  
C:Genetics:  
A:Gene: IgG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 78.0%; Score 458; DB 2; Length 328;  
Best Local Similarity 78.8%; Pred. No. 4.1e-38;  
Matches 82; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
QY 7 GPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKPREQY 66  
DB 116 GPSVFIFPPPKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKPREQY 175  
QY 67 NSTYRVSVLTVLHQDLNGLKEPKYCKVSNKGLPSSIEKTIISKAK 110  
DB 176 NSTYRVSVLPIQHODWLNGLKEPKYCKVSNKGLPAPITRIISKAK 219  
RESULT 12  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47162  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47162  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-277 <KAC>  
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130  
C:Genetics:  
A:Gene: IgG4  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:182-151/Domain: immunoglobulin homology <IMM>  
Query Match 77.2%; Score 453; DB 2; Length 277;  
Best Local Similarity 77.9%; Pred. No. 1e-37;  
Matches 81; Conservative 14; Mismatches 9; Indels 0; Gaps 0;  
QY 7 GPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKPREQY 66  
DB 65 GPSAFIFPPPKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKPREQY 124  
QY 67 NSTYRVSVLTVLHQDLNGLKEPKYCKVSNKGLPSSIEKTIISKAK 110  
DB 125 NSTYRVSVLPIQHODWLNGLKEPKYCKVSNKGLPAPITRIISKAK 168  
RESULT 13  
S22080  
Ig heavy chain precursor (B/Mt.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G440  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gam  
A:Reference number: S06610; MUID:90097956; PMID:2513487  
A:Accession: S06610  
A:Molecule type: DNA  
A:Residues: 142-470 <SYM>  
A:Cross-references: EMBL:X16701  
A:Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Gene: Ig CH gamma-1  
A:Introns: 98/1; 111/1; 221/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F:161-225/Domain: immunoglobulin homology <IMM>  
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 75.0%; Score 440; DB 2; Length 470;  
Best Local Similarity 72.5%; Pred. No. 3.9e-36;  
Matches 79; Conservative 13; Mismatches 17; Indels 0; Gaps 0;  
QY 2 PPVAGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKP 61  
DB 253 PELPGPSVFIFFPKPKDTLTISGTPEVTCVVDVSHDEPEVKFNWYVDGVVHNAKTKP 312  
QY 62 REEQNSTYRVSVLTVLHQDLNGLKEPKYCKVSNKGLPSSIEKTIISKAK 110  
DB 313 REEQNSTYRVSVLPIQHODWLNGLKEPKYCKVSNKGLPAPITRIISKAK 361  
RESULT 14  
I47161  
Ig gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.

Search completed: April 29, 2004, 08:46:57  
Job time : 13.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: April 29, 2004, 08:37:47 ; Search time 10 seconds  
(without alignments)  
572.772 Million cell updates/sec

Title: US-09-674-857-3  
Perfect score: 587  
Sequence: 1 APPVAGGPSVFLFPKPKDT.....CKVSNKGLPSSIENTISKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	94.9	330	GCI_HUMAN	P01857 homo sapien
2	553	94.2	327	GQ4_HUMAN	P01861 homo sapien
3	543.5	92.6	326	GQ2_HUMAN	P01859 homo sapien
4	519	88.4	290	GQ3_HUMAN	P01860 homo sapien
5	431	73.4	333	GCE_RAT	P20761 rattus norv
6	421	71.7	323	GC_RABIT	P01870 oryctolagus
7	421	71.7	329	GQ2_CAVPO	P01862 cavia porce
8	418	71.2	329	GQ3_MOUSE	P22436 mus musculu
9	418	71.2	398	GQ3_MOUSE	P03987 mus musculu
10	397	67.6	336	GCB_MOUSE	P01866 mus musculu
11	397	67.6	405	GCB_MOUSE	P01867 mus musculu
12	396	67.5	324	GCI_MOUSE	P01868 mus musculu
13	396	67.5	329	GCC_RAT	P20762 rattus norv
14	396	67.5	393	GCI_MOUSE	P01869 mus musculu
15	394	67.1	335	GCA_MOUSE	P01864 mus musculu
16	391	66.6	330	GCA_MOUSE	P01863 mus musculu
17	391	66.6	399	GCA_MOUSE	P01865 mus musculu
18	380	64.7	326	GCI_RAT	P20759 rattus norv
19	339	57.8	322	GCA_RAT	P20760 rattus norv
20	166.5	28.4	428	EPC_HUMAN	P01854 homo sapien
21	153	26.1	429	EPC_RAT	P01855 rattus norv
22	153	26.1	457	MUC_SUNMU	P20768 suncus muri
23	138	23.5	421	EPC_MOUSE	P06336 mus musculu
24	138	23.5	454	MUC_HUMAN	P01871 homo sapien
25	137.5	23.4	299	ALC_RABIT	P01879 oryctolagus
26	136	23.2	391	MUCB_HUMAN	P04220 homo sapien
27	132	22.5	454	MUC_MESAU	P06337 mesocricetu
28	132	22.5	455	MUC_MOUSE	P01872 mus musculu
29	132	22.5	476	MUC_MOUSE	P01873 mus musculu
30	131	22.3	106	KAC_HUMAN	P01834 homo sapien
31	130	22.1	193	LAC_CHICK	P20763 gallus gall
32	125	21.3	450	MUC_CANFA	P01874 canis famil
33	121.5	20.7	105	LAC_MOUSE	P01843 mus musculu

34	121.5	20.7	105	1	LACS_MUSSP	P20765 mus spretus
35	120	20.4	458	1	MUC_RABIT	P03988 oryctolagus
36	120	20.4	479	1	MUC_RABIT	P04221 oryctolagus
37	118.5	20.4	340	1	ALC3_HUMAN	P01877 homo sapien
38	119.5	20.4	353	1	ALC3_GORGO	P20758 gorilla gor
39	119.5	20.4	353	1	ALC1_HUMAN	P01876 homo sapien
40	117.5	20.0	105	1	LACS_MOUSE	P20764 mus musculu
41	112	19.1	103	1	KAC4_RABIT	P01840 oryctolagus
42	111.5	19.0	344	1	HVC3_MOUSE	P01878 mus musculu
43	111.5	19.0	393	1	HVC3_HETFR	P23086 heterodontu
44	110.5	18.8	213	1	ILL3_HUMAN	P15814 homo sapien
45	109.5	18.7	105	1	LAC_HUMAN	P01842 homo sapien

ALIGNMENTS

RESULT 1  
GCI\_HUMAN  
ID GCI\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN IGHG1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Barson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064025; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Maxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIB).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=684994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196 (1970).  
RP [7]  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Delsenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370 (1981).  
CC -!- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC GIM(3) marker and the GIM (non-1) markers.  
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of  
CC 35, 116, 198, 269 and 272.  
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
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CC -----  
DR EXBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A93433; GHU.  
DR PDB; 1PC1; 15-JUL-92.  
DR PDB; 1PC2; 15-JUL-92.  
DR PDB; 1AJ7; 12-NOV-97.  
DR PDB; 1D5B; 09-FEB-00.  
DR PDB; 1D51; 09-FEB-00.  
DR PDB; 1D6V; 04-OCT-00.  
DR PDB; 1DN2; 17-MAY-00.  
DR PDB; 1E4K; 06-JUN-01.  
DR PDB; 1FCC; 28-JUL-95.  
DR PDB; 1H2Z; 12-JUN-02.  
DR PDB; 1I1S; 08-AUG-01.  
DR PDB; 1I1X; 16-MAY-01.  
DR PDB; 1L6X; 10-APR-02.  
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DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; -.  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGH1; 2.  
DR PROSITE; PS00835; IG LIKE; 3.  
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DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure. 1  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CHI.  
FT HINGE 110  
FT DOMAIN 111 223 HINGE.  
FT CH2.

DOMAIN 224 330  
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DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
DISULFID 144 204  
DISULFID 250 308  
CARBOHYD 180 180  
MOD RES 330 330  
VARIANT 97 97  
VARIANT 239 239  
VARIANT 241 241  
STRAND 122 126  
HELIX 130 134  
TURN 136 137  
STRAND 141 147  
STRAND 157 162  
TURN 163 164  
STRAND 165 166  
TURN 168 171  
STRAND 176 179  
TURN 180 181  
STRAND 182 190  
HELIX 193 197  
TURN 198 199  
STRAND 202 207  
TURN 209 210  
STRAND 215 219  
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HELIX 238 242  
STRAND 245 256  
STRAND 260 265  
STRAND 270 270  
STRAND 274 276  
STRAND 280 281  
TURN 283 284  
STRAND 287 295  
HELIX 297 301  
TURN 302 303  
STRAND 305 312  
TURN 313 314  
TURN 316 317  
STRAND 320 325  
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Best Local Similarity 94.5%; Pred. No. 5.2e-49;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 APPVAGGSPVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 114 APPELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVKNKGLPSSIEKTISKAK 110  
Db 174 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVKNKGLPSSIEKTISKAK 223  
RESULT 2  
GC4\_HUMAN  
ID GC4\_HUMAN STANDARD; PRT; 327 AA.  
AC P01861;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig gamma-4 chain C region.  
GN IGHG4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=83157104; PubMed=6299662;
RX Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18 (1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47 (1970).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1A0Q; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_WHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TER 1 1
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CHI.
FT DOMAIN 221 327 CHI.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;
Query Match 94.2%; Score 553; DB 1; Length 327;
Best Local Similarity 94.5%; Pred.No.1.3e-48;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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DB 111 APEFLGGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTK 170
QY 61 PREEQNSTYRVYVSLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAK 110
DB 171 PREEQNSTYRVYVSLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAK 220
RESULT 3
GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988 (1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RA MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679 (1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RA MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407 (1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung B., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054 (1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767 (1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925 (1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RA J. Biochem. 228:886-893 (1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225 (1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";

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RL Nature 221:145-148(1969).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A93906; G2HU.
DR HSSP; P01857; IFC1.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147120; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SMO0407; IGC1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 219
FT DOMAIN 220 326
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 92.6%; Score 543.5; DB 1; Length 326;
Best Local Similarity 92.7%; Pred. No. 1.2e-47;
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 111 APPVA-GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 169

Qy 61 PREEQYNSTYVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 170 PREQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTIKTK 219

RESULT 4
ID GC3 HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE IG gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]

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RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL gamma 3 heavy-chain disease protein Wis.",
RN Biochemistry 19:4304-4308(1980).
RP REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RL quadruplication of a 15-amino acid residue basic unit.",
RN J. Biol. Chem. 252:893-899(1977).
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RL Structure of the FC fragment of immunoglobulin G3.",
RN Biochem. Biophys. Res. Commun. 71:907-914(1976).
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barztaut D., Frangione B.,
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RL gene deletion model.", U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC interchain disulfide bond at position 7 in addition to the 11
CC normally present in the hinge region.
CC -1- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC Ref. 2.
CC -1- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC and all of the CH1 region.
CC -1- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC of the CH1 region, and part of the hinge compared with normal
CC gamma-3 heavy chains.
CC -1- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC or another gamma chain subclass.
CC -1- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC times as long as in other gamma chains and contains three
CC identical 15-residue segments preceded by a similar 17-residue
CC segment (12-28).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00231; AAB52805.1; ALT_SEQ.
DR HSSP; P01857; IFC1.
DR Genew; HGNC:5527; IGHG3.
DR MIM; 147120; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SMO0407; IGC1; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW Pyridone carboxylic acid.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.

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FT REPEAT 29 43  
 FT REPEAT 44 58  
 FT REPEAT 59 73  
 FT MOD RES 1 1  
 FT CARBOHYD 6 6  
 FT DISULFID 7 7  
 FT DISULFID 24 24  
 FT DISULFID 27 27  
 FT DISULFID 33 33  
 FT DISULFID 39 39  
 FT DISULFID 42 42  
 FT DISULFID 48 48  
 FT DISULFID 54 54  
 FT DISULFID 57 57  
 FT DISULFID 63 63  
 FT DISULFID 69 69  
 FT DISULFID 72 72  
 FT CARBOHYD 140 140  
 FT MOD RES 290 290  
 FT VARIANT 126 127  
 FT VARIANT 134 134  
 FT VARIANT 139 139  
 FT VARIANT 182 182  
 FT VARIANT 227 227  
 FT VARIANT 227 227  
 FT VARIANT 279 279  
 SQ SEQUENCE 290 AA; 32331 MW; E69BC95705B2F46 CRC64;  
 Query Match 88.4%; Score 519; DB 1; Length 290;  
 Best Local Similarity 86.4%; Pred. No. 3.1e-45;  
 Matches 95; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
 DB 74 APPLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 133  
 QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 134 PREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKTK 183  
 RESULT 5  
 GCB\_RAT  
 ID\_GCB\_RAT STANDARD; PRT; 333 AA.  
 AC P20761;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-2B chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;  
 RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";  
 RL Gene 74:473-482(1988).  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 DR PIR; PS0018; PS0018.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_YHC.  
 DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 96 IG-LIKE 1.  
 FT DOMAIN 124 223 IG-LIKE 2.  
 FT DOMAIN 232 328 IG-LIKE 3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 147 207  
 FT DISULFID 253 311  
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;  
 Query Match 73.4%; Score 431; DB 1; Length 333;  
 Best Local Similarity 69.7%; Pred. No. 2.9e-36;  
 Matches 76; Conservative 19; Mismatches 14; Indels 0; Gaps 0;  
 QY 2 PPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61  
 DB 118 PELLGGPSVFLPPPKKDTLLISQAKVTCVVVDVSEEPDVFQSFVNNVEVHTAQTP 177  
 QY 62 RSEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 178 RSEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKTKP 226  
 RESULT 6  
 GCB\_RABIT  
 ID\_GCB\_RABIT STANDARD; PRT; 323 AA.  
 AC P01870;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma chain C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84030930; PubMed=6313520;  
 RA Bernstein K.E., Alexander C.B., Mage R.G.;  
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplotype.";  
 RL Immunogenetics 18:387-397(1983).  
 RN [2]  
 RP SEQUENCE OF 1-128.  
 RX MEDLINE=76135469; PubMed=1243651;  
 RA Pratt D.M., Mole L.E.;  
 RT "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";  
 RL Biochem. J. 151:337-349(1975).  
 RN [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=83299917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 RN [4]  
 RP SEQUENCE OF 132-161.  
 RX MEDLINE=70110015; PubMed=5461106;  
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.";  
 RL Biochem. J. 116:249-259(1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.

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RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Klander J. (eds.);
RL Gamma globulins, Nobel Symp. 3, pp.109-127, Almqvist and Wiksell,
CC Stockholm (1967).
CC -1- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
CC markers and Ref.5 the E15 marker.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A91743; GHBB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON TER 1
FT DOVAIN 6 96 IG-LIKE 1.
FT DOVAIN 114 213 IG-LIKE 2.
FT DOVAIN 222 318 IG-LIKE 3.
FT VARIANT 104 104 T -> W (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 E -> Q (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 E -> G (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 71.7%; Score 421; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 2.9e-35;
Matches 76; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 2 PPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 108 PELLGGPSVFIPEPKKDTLMISRTPEVTCVVVDVSDPEVQFTWVNNQVETARPPL 167

Qy 62 REEOVNSTYRVSVLTIVLHODLWNGKYCKVSKNGLPSSIEKTIISKAK 110
Db 168 REQQFNSTIRVSTLPITHQDLWLRGKGFCKCKVHNAKLPAPIETKISKAR 216

RESULT 7
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]_TaxID=10141;
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birestein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 71.7%; Score 421; DB 1; Length 329;
Best Local Similarity 71.6%; Pred. No. 2.9e-35;
Matches 78; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 2 PPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 113 PENLGGPSVFIPEPKKDTLMISRTPEVTCVVVDVSDPEVQFTWVNNQVETARPPL 172

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QY 62 RESQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110  
Db 173 RVSQNTTFRVSVLPQHODWLNKGYCKVSNKGLPSSIEKTIKAK 221

RESULT 8  
GC3M MOUSE  
ID GC3M MOUSE STANDARD; PRT; 329 AA.  
AC P22436;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-3 chain C region, secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Sutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN 11;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85027161; PubMed=6092053;  
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
RA Tucker P.W., Blattner F.R.;  
RT "Structural analysis of the murine IgG3 constant region gene";  
RL EMOB J. 3:2041-2046(1984).  
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CC  
CC EMBL; J00451; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; J00451; -; NOT\_ANNOTATED\_CDS.  
DR PIR; B02156; G3MSC.  
DR HSSP; P01857; 1FC1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IG1; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Transmembrane; Alternative splicing.  
FT NON TER 1 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 113 HINGE.  
FT DOMAIN 114 223 CH2.  
FT DOMAIN 224 327 CH3.  
FT TRANSMEM 346 362  
FT DOMAIN 363 398  
FT CONFLICT 333 333  
FT CONFLICT 342 342  
FT CONFLICT 388 388  
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;  
Query Match 71.2%; Score 418; DB 1; Length 329;  
Best Local Similarity 68.5%; Pred. No. 5.9e-35;  
Matches 76; Conservative 15; Mismatches 18; Indels 2; Gaps 1;  
QY 2 PP--VAGGSPVFLPPPKPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 59  
Db 112 PPGNILGGPSVFIPPPKPKDMLSLTPKVTCTVVDVSEDDPDVHVSFWVDNKEVHTAWT 171

QY 60 KPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110  
Db 172 QPREAQNSTFRVVSALPIQHODWLNKGYCKVSNKGLPSSIEKTIKAK 222

RESULT 9  
GC3M MOUSE  
ID GC3M MOUSE STANDARD; PRT; 398 AA.  
AC P03987;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-3 chain C region, membrane-bound form.

QY 62 RESQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110  
Db 173 RVSQNTTFRVSVLPQHODWLNKGYCKVSNKGLPSSIEKTIKAK 221

RESULT 10  
GC3M MOUSE  
ID GC3M MOUSE STANDARD; PRT; 336 AA.  
AC P01866;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ig gamma-2B chain C region secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
EN [1]  
RP SEQUENCE FROM N.A. (ALLELE A).  
RX MEDLINE=86120716; PubMed=6766534;  
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;  
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene  
cloned from newborn mouse DNA.";  
RL Nature 283:786-789(1980).  
RN [2]  
RP SEQUENCE FROM N.A. (NPC 11).  
RX MEDLINE=80081501; PubMed=117548;  
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;  
RT "Structure of the constant and 3' untranslated regions of the murine  
gamma 2b heavy chain messenger RNA.";  
RL Science 206:1299-1303(1979).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80081502; PubMed=117549;  
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;  
RT "Sequence of the cloned gene for the constant region of murine gamma  
2b immunoglobulin heavy chain.";  
RL Science 206:1303-1306(1979).  
RN [4]  
RP SEQUENCE FROM N.A. (ALLELE B).  
RX MEDLINE=82173203; PubMed=6603173;  
RA Ollio R., Rougeon F.;  
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma  
2a and gamma 2b chain genes.";  
RL Nature 296:761-763(1982).  
RN [5]  
RP CA3OHYDRATE-LINKAGE SITE THR-105.  
RX MEDLINE=94216359; PubMed=7512967;  
RA Kim H., Yamaguchi Y., Masuda C., Matsunaga C., Yamamoto K.,  
RA Irimura T., Takahashi N., Kato K., Arata Y.;  
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";  
RL J. Biol. Chem. 269:12345-12350(1994).  
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Secreted;  
CC Note=May be the major isoform;  
CC IsoId=P01866-1; Sequence=Displayed;  
CC Name=Membrane-bound;  
CC IsoId=P01867-1; Sequence=External;  
CC -1- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS  
MODIFIED WITH 2 SIALIC ACID RESIDUES.  
CC -1- PTM: DISULFIDE BONDS BY HOMOLOG WITH OTHER IG GAMMA CHAINS.  
CC -1- MISCELLANEOUS: The a allele sequence is shown.  
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
DR PIR: S25057; G2MS11.  
DR HSSP: P01842; 7FAB.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig\_c1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 3.  
DR SMART: SM00407; IGL1; 2.  
DR PROSITE: PS00835; IG LIKE; 3.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing; Repeat.  
FT NON TER 1 1  
FT DOMAIN 6 98 IG-LIKE 1.  
FT DOMAIN 127 226 IG-LIKE 2.  
FT DOMAIN 235 331 IG-LIKE 3.  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 150 210  
FT DISULFID 256 314  
FT CARBOHYD 105 105  
FT MOD RES 336  
FT VARIANT 163  
FT VARIANT 194  
FT VARIANT 300  
FT VARIANT 301  
FT CONFLICT 25  
FT CONFLICT 36  
FT CONFLICT 239  
FT CONFLICT 336  
SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356B CRC64;  
Query Match 67.6%; Score 397; DB 1; Length 336;  
Best local similarity 65.5%; Pred. No. 8e-33;  
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;  
QY 1 APPVAGSPVELPPPKPKDTLMISRTPEVTCVVYVSHEDPEVKFVYVGVVHNAKTK 60  
DB 120 APNLEGGSPVFIFFPNKIDVLMISLTPKVCVVVDSEDDPDVQISFWVNNVSVHTAQ 179  
QY 61 PREEQYNTRYVSVLTIVLHQLNGKYEKCKVKNKGLPSSIEKTKSKAK 110  
DB 180 THREDYNSTIRVVSTLPIQHDMWMSGKFKCKVKNKGLPSPERTISKIK 229  
RESULT 11  
GCEN MOUSE  
ID GCEN MOUSE STANDARD; PRT; 405 AA.  
AC P01867;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ig gamma-2B chain C region, membrane-bound form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE OF 335-405 FROM N.A.  
RX MEDLINE=82222190; PubMed=6283537;  
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of  
immunoglobulin gamma chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
RN [2]  
RP SEQUENCE OF 335-378 FROM N.A.  
RX MEDLINE=82115295; PubMed=6799207;  
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
RA Eisenberg D., Wall R.;  
RT "Gene segments encoding transmembrane carboxyl termini of  
immunoglobulin gamma chains.";  
RL Cell 26:19-27(1981).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Membrane-bound;  
CC IsoId=P01867-1; Sequence=Displayed;  
CC Name=Secreted;  
CC IsoId=P01866-1; Sequence=External;  
CC Note=May be the major isoform;  
CC -1- PTM: DISULFIDE BONDS BY HOMOLOG WITH OTHER IG GAMMA CHAINS.  
CC -1- MISCELLANEOUS: The sequence of residues 1-335 is assumed to be  
identical with the corresponding region of the secreted form.  
CC -1- MISCELLANEOUS: The a allele sequence is shown.  
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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EMBL; J00462; AAB59659.1; ALT\_INIT.  
 PIR; C02154; G2MSBM.  
 PDB; 1CIC; 11-MAR-03.  
 MGD; MGI:96445; Igh-3.  
 InterPro; IPR007110; Igh-like.  
 InterPro; IPR003597; Igh cl.  
 InterPro; IPR003006; Igh\_MEC.  
 Pfam; PF00047; Igh; 3.  
 SMART; SM00407; Igc1; 2.  
 PROSITE; PS00835; IGH LIKE; 3.  
 PROSITE; PS00290; IGH\_MHC; 1.  
 Immunoglobulin domain; Immunoglobulin C region; Transmembrane;  
 Alternative splicing; 3D-structure; Repeat.  
 NON\_TER 1  
 DOMAIN 6 98  
 DOMAIN 127 226  
 DOMAIN 235 331  
 DISULFID 15 15  
 DISULFID 27 82  
 DISULFID 109 109  
 DISULFID 112 112  
 DISULFID 115 115  
 DISULFID 118 118  
 DISULFID 150 210  
 DISULFID 256 314  
 TRANSMEM 352 369  
 DOMAIN 370 405  
 SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 Query Match 67.6%; Score 397; DB 1; Length 405;  
 Best Local Similarity 65.5%; Pred. No. 9.9e-33;  
 Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDSVSHEDPEVKFNHYVDGVEVENAKTK 60  
 Db 120 APNLEGGSPVFPFNPNTKDLKLSLTPKVTCCVVDVSEDDPDQVQISWFMNVNVEVHTAQTK 179  
 Qy 61 PREQYNTSRVWSVLTPLHQDMLNGKEYCKVSKNGKLPSSIEKTIKSKAK 110  
 Db 180 THREDYNSIRVSTPLTQHQDMSGKEFKCKVANKDLPSSIEKTIKSKIK 229  
 RESULT 12  
 GC1\_MOUSE  
 ID GC1\_MOUSE STANDARD; PRT; 324 AA.  
 AC P01868;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Igh gamma-1 chain C region secreted form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80045036; PubMed=115593;  
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 RT gamma 1 chain gene."  
 RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
 RX MEDLINE=80202559; PubMed=6769752;  
 RA Obata Y., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
 RT cloned in a bacterial plasmid."  
 RL Gene 9:87-97(1980).  
 RN [3]

SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
 MEDLINE=80012837; PubMed=113776;  
 Rogers J., Clarke P., Salsner W.;  
 "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
 heavy chain."  
 Nucleic Acids Res. 6:3305-3321(1979).  
 [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=78242288; PubMed=98524;  
 Adegugbo K.;  
 "Evolution of immunoglobulin subclasses. Primary structure of a  
 murine myeloma gamma chain."  
 J. Biol. Chem. 253:6068-6075(1978).  
 [5]  
 RP DISULFIDE BONDS (MOPC 21).  
 RX MEDLINE=73008889; PubMed=5073237;  
 Svasti J., Milstein C.;  
 "The disulphide bridges of a mouse immunoglobulin G1 protein."  
 Biochem. J. 126:837-850(1972).  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Secreted;  
 CC IsoId=P01868-1; Sequence=Displayed;  
 CC Note=May be the major isoform;  
 CC Name=Membrane-bound;  
 CC IsoId=P01869-1; Sequence=External;  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
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 CC EMBL; V00793; CAA24172.1; -;  
 CC EMBL; V00793; CAA24173.1; -;  
 CC EMBL; V00793; CAA24174.1; -;  
 CC EMBL; V00793; CAA24175.1; -;  
 CC EMBL; V00793; CAA24176.1; -;  
 CC PIR; A02159; GIMS.  
 CC GlycoSuiteDB; P01868; -;  
 CC MGD; MGI:96446; Igh-4.  
 CC InterPro; IPR007110; Igh-like.  
 CC InterPro; IPR003597; Igh cl.  
 CC InterPro; IPR003006; Igh\_MHC.  
 CC Pfam; PF00047; Igh; 2.  
 CC SMART; SM00407; Igc1; 2.  
 CC PROSITE; PS00835; IGH LIKE; 3.  
 CC PROSITE; PS00290; IGH\_MHC; 1.  
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 CC Alternative splicing.  
 CC NON\_TER 1 1  
 CC DOMAIN 1 97  
 CC DOMAIN 98 110  
 CC DOMAIN 111 217  
 CC DOMAIN 218 324  
 CC DOMAIN 27 82  
 CC DISULFID 102 102  
 CC DISULFID 104 104  
 CC DISULFID 107 107  
 CC DISULFID 109 109  
 CC DISULFID 138 198  
 CC CARBOHYD 174 174  
 CC INTERCHAIN (WITH A LIGHT CHAIN).  
 CC INTERCHAIN (WITH A HEAVY CHAIN).  
 CC INTERCHAIN (WITH A HEAVY CHAIN).  
 CC N-LINKED (GLCNAC. . .).  
 CC /FTIG=CAR\_000055.  
 CC  
 CC DISULFID 244 302  
 CC MOD\_RES 324 324  
 CC CONFLICT 276 276  
 CC CONFLICT 278 278  
 CC SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
 Query Match 67.5%; Score 396; DB 1; Length 324;





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:02 ; Search time 36 Seconds  
(without alignments)  
964.083 Million cell updates/sec

Title: US-09-674-857-3  
Perfect score: 587  
Sequence: 1 APPVAGGPSVFLPPPKPDKT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

17	382	65.1	468	11	Q99L31	Q99L31 mus musculus
18	382	65.1	473	11	Q99L25	Q99L25 mus musculus
19	138	23.5	375	4	Q86TT1	Q86TT1 homo sapien
20	138	23.5	588	4	Q8WUX4	Q8WUX4 homo sapien
21	138	23.5	597	4	Q8BUI0	Q8BUI0 homo sapien
22	138	23.5	597	4	Q8QOB8	Q8QOB8 homo sapien
23	138	23.5	597	4	Q8EBB9	Q8EBB9 homo sapien
24	138	23.5	613	4	Q86EY0	Q86EY0 homo sapien
25	138	23.5	613	4	Q8WUK1	Q8WUK1 homo sapien
26	138	23.5	614	4	Q86GAG	Q86GAG homo sapien
27	138	23.5	618	4	Q86AA6	Q86AA6 homo sapien
28	132	22.5	613	11	Q8VCX7	Q8VCX7 mus musculus
29	132	22.5	614	11	Q7TWT6	Q7TWT6 mus musculus
30	131	22.3	234	4	Q7Z473	Q7Z473 homo sapien
31	131	22.3	236	4	Q7Z4Y4	Q7Z4Y4 homo sapien
32	131	22.3	239	4	Q8NEK0	Q8NEK0 homo sapien
33	131	22.3	239	4	Q8TCD0	Q8TCD0 homo sapien
34	123.5	21.0	478	4	Q7Z379	Q7Z379 homo sapien
35	122.5	20.9	684	13	Q90544	Q90544 ginglymosto
36	121.5	20.7	130	11	Q9D8W4	Q9D8W4 mus musculus
37	120	20.4	497	4	Q8W124	Q8W124 homo sapien
38	119.5	20.4	384	4	Q9UP60	Q9UP60 homo sapien
39	119.5	20.4	416	4	Q9NPP6	Q9NPP6 homo sapien
40	119.5	20.4	492	4	Q7Z374	Q7Z374 homo sapien
41	119.5	20.4	493	4	Q8NCL6	Q8NCL6 homo sapien
42	119.5	20.4	494	4	Q9EK68	Q9EK68 homo sapien
43	119.5	20.4	496	4	Q96DK0	Q96DK0 homo sapien
44	119.5	20.4	496	4	Q96KX8	Q96KX8 homo sapien
45	119.5	20.4	499	4	Q8N5K4	Q8N5K4 homo sapien

ALIGNMENTS

RESULT 1

Q7Z7P5 PRELIMINARY; PRT; 469 AA.

AC Q7Z7P5; TREMBLrel. 25, Created

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1] TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	557	94.9	469	4	Q7Z7P5	Q7Z7P5 homo sapien
2	557	94.9	470	4	Q7Z5W1	Q7Z5W1 homo sapien
3	557	94.9	482	4	Q7Z351	Q7Z351 homo sapien
4	557	94.9	675	4	Q9EPQ8	Q9EPQ8 homo sapien
5	553	94.2	473	4	Q8TC63	Q8TC63 homo sapien
6	539	91.8	354	4	Q86TT2	Q86TT2 homo sapien
7	539	91.1	509	4	Q8NF17	Q8NF17 homo sapien
8	535	91.1	531	4	Q8N4V9	Q8N4V9 homo sapien
9	458	78.0	337	6	Q95M34	Q95M34 equus caball
10	448	71.2	470	11	Q7TWT6	Q7TWT6 mus musculus
11	400	68.1	469	11	Q8R3V9	Q8R3V9 mus musculus
12	397	67.6	473	11	Q91Z05	Q91Z05 mus musculus
13	397	67.6	474	11	Q8R3H6	Q8R3H6 mus musculus
14	396	67.5	437	11	Q9R1A4	Q9R1A4 mus musculus
15	396	67.5	463	11	Q93EC4	Q93EC4 mus musculus
16	394	67.1	473	11	Q9DBL4	Q9DBL4 mus musculus

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Db      314 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 363
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RESULT 3
Q7Z351 PRELIMINARY; PRT; 482 AA.
ID Q7Z351
AC Q7Z351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFP686N02209.
DE DKFP686N02209.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX538118; CAD98026.1; -.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F19D1A034 CRC64;
Query Match 94.9%; Score 557; DB 4; Length 482;
Best Local Similarity 94.5%; Pred. NO. 9.3e-54;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 APPVAGGSPGVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHAKTK 60
|||
DB 266 ABEILGGSPGVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHAKTK 325
|||||
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 110
|||||
DB 326 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 375
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RESULT 4
Q96F08 PRELIMINARY; PRT; 679 AA.
ID Q96F08
AC Q96F08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Factor VII active site mutant immunocojugate.
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
[2]
RN SEQUENCE FROM N.A.
RC Hu Z., Garen A.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF272774; AAKS8686.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Axx_hydroxyl_S.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006742; EGF 2.
DR InterPro; IPR001881; EGF Ca.

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DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0010; EGF_blood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA_1.
DR PROSITE; PS00031; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 679 AA; 75552 MW; 080023AE70A067A1 CRC64;

Query Match 94.9%; Score 557; DB 4; Length 679;
Best Local Similarity 94.5%; Pred. No. 1.4e-53;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60
Db 463 APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 522

Qy 61 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 523 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 572

RESULT 5
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RT "Full-length cDNA libraries and normalization."
DR EMBL; BC025985; AAH25985.1;
DR GO; GO:0005507; F.copper ion binding; IEA.
DR GO; GO:0005489; F.electron transporter activity; IEA.
DR GO; GO:0006118; F.electron transport; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.

Query Match 94.2%; Score 553; DB 4; Length 473;
Best Local Similarity 94.5%; Pred. No. 2.6e-53;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60
Db 257 APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 316

Qy 61 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 317 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 366

RESULT 6
Q86TT2 PRELIMINARY; PRT; 354 AA.
AC Q86TT2;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CS0D1019F20 of Placenta of Homo sapiens (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization."
DR EMBL; BX248278; CAD62606.1;
DR GO; GO:0046821; C.extrachromosomal DNA; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;

Query Match 91.8%; Score 539; DB 4; Length 354;
Best Local Similarity 90.9%; Pred. No. 6.6e-52;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60
Db 138 APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 197

Qy 61 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 198 PREEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 247

RESULT 7
Q8NF17 PRELIMINARY; PRT; 509 AA.
ID Q8NF17

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AC Q8NF17;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE FLJ00385 protein (Fragment).  
 GN FLJ00385.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;  
 RT "The nucleotide sequence of a long cDNA clone isolated from human spleen."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK090464; BAC03445.1; --  
 DR PIR; A45874; A45874. Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGC1; 3.  
 DR PROSITE; PS00835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 FT NON\_TER 1  
 SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match 91.1%; Score 535; DB 4; Length 509;  
 Best Local Similarity 90.0%; Pred. No. 2.9e-51;  
 Matches 99; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTK 60  
 DB 224 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTK 283  
 QY 61 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVKNKGLPSSIEKTIKSKAK 110  
 DB 284 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVKNKGLPSSIEKTIKSKAK 333

RESULT 8  
 Q8N4Y9  
 ID Q8N4Y9 PRELIMINARY; PRT; 521 AA.  
 AC Q8N4Y9;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC033178; AAH333178.1; --  
 DR PIR; A50764; A50764.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 91.1%; Score 535; DB 4; Length 521;  
 Best Local Similarity 90.0%; Pred. No. 3e-51;  
 Matches 99; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTK 60  
 DB 305 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTK 364  
 QY 61 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVKNKGLPSSIEKTIKSKAK 110  
 DB 365 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVKNKGLPSSIEKTIKSKAK 414

RESULT 9  
 Q95M34  
 ID Q95M34 PRELIMINARY; PRT; 337 AA.  
 AC Q95M34;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).  
 GN IGHC1.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wagner B.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98383416; PubMed=9717671;  
 RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
 RA Leibold W., Radbruch A.;  
 RT "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."  
 RL Immunobiology 199; 105-119 (1998).  
 DR EMBL; AJ300675; CAC44624.1; --  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00407; IGC1; 2.  
 DR PROSITE; PS00835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 FT NON\_TER 1  
 SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1P6 CRC64;

Query Match 78.0%; Score 458; DB 6; Length 337;  
 Best Local Similarity 73.6%; Pred. No. 7.4e-43;  
 Matches 81; Conservative 16; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTK 60  
 DB 119 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTK 178  
 QY 61 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVKNKGLPSSIEKTIKSKAK 110  
 DB 179 PREEQNSTYRVSVLTVLHQLDNLNGKEYCKVKNKGLPSSIEKTIKSKAK 228

RESULT 10  
 Q7TMK1  
 ID Q7TMK1 PRELIMINARY; PRT; 470 AA.  
 AC Q7TMK1;  
 DT 01-OCT-2003 (TREMblrel. 25, Created)  
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MDLINE=22398257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zebins R., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC055910; AAH55910.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 71.2%; Score 418; DB 11; Length 470;
Best Local Similarity 68.5%; Pred. No. 3.4e-36;
Matches 76; Conservative 15; Mismatches 18; Indels 2; Gaps 1;

QY 2 PP--VAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
DB 253 PPGNLLGGSPVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
QY 60 KPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
DB 313 QPREAQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 313

RESULT 11
Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC024405; AAH24405.1; -.
DR PIR; B45837; B45837.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF000047; Igh_3.
DR SMART; SM00406; Igh; 1.
DR PROSITE; PS00835; IGH_LIKE; 4.
DR PROSITE; PS00290; IGH_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625P008932AP12 CRC64;

Query Match 67.6%; Score 397; DB 11; Length 473;
Best Local Similarity 65.5%; Pred. No. 7.6e-36;
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 60
DB 257 ANLEGGSPVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 60
QY 61 PREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
DB 317 THREDYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 366

RESULT 13
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; SC025447; AAH25447.1; -  
DR MGD; MGI:2144567; AU044919.  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR SMART; PF00047; Ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00190; CYTOCHROME C; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;  
  
Query Match 67.5%; Score 397; DB 11; Length 474;  
Best Local Similarity 65.5%; Pred. No. 7.6e-36;  
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;  
  
OY 1 APPVAGGSVFPPKPKDMLISPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 258 APNLEGGSPVFIPPNIKDKVLMISPTPKVTCVVVDVSHEDDPQVQISFNWVVEVHTAQ 317  
OY 61 PREEQNSYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 318 THREDYNSTIRVVSALPIQHDQMSGKEPKCKVNNKDLPSPIERTISKIK 367  
  
RESULT 14  
Q9RIA4  
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.  
AC Q9RIA4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
GN Gamma1 heavy chain of Mab7 (fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
antibody (Mab 7, its light and heavy chains) and construction of a  
single chain antibody (scFv)".  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152372; AA040243.1; -  
DR PIR; B45837; B45837.  
DR PDB; 1CQK; 11-SEP-99.  
DR PDB; 1I9I; 25-DEC-02.  
DR PDB; 1KCU; 11-MAY-02.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 437  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;

Query Match 67.5%; Score 396; DB 11; Length 437;  
Best Local Similarity 67.6%; Pred. No. 8.9e-36;  
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;  
  
OY 9 SVFLFPKPKDMLISPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 68  
DB 229 SVFIFFPKPKDVLITITPKVTCVVVDISKDDPEVQSFVDDVEVHTAQTPREEQVNS 288  
OY 69 TYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 289 TFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEKTISKTK 330  
  
RESULT 15  
Q99LCA  
ID Q99LCA PRELIMINARY; PRT; 463 AA.  
AC Q99LCA;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to RIKEN cDNA 1810060009 gene.  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003435; AA003435.1; -  
DR PIR; B45837; B45837.  
DR HSSP; P01842; 7FAB.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;  
  
Query Match 67.5%; Score 396; DB 11; Length 463;  
Best Local Similarity 67.6%; Pred. No. 9.6e-36;  
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;  
  
OY 9 SVFLFPKPKDMLISPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 68  
DB 255 SVFIFFPKPKDVLITITPKVTCVVVDISKDDPEVQSFVDDVEVHTAQTPREEQVNS 314  
OY 69 TYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 315 TFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEKTISKTK 356  
  
Search completed: April 29, 2004, 08:46:18  
Job time : 37 secs

OM protein - protein search, using sw model

Run on: April 23, 2004, 08:46:23 ; Search time 38.5 Seconds  
(without alignments)  
791.970 Million cell updates/sec

Title: US-09-674-857-3  
Perfect score: 587  
Sequence: 1 APPVAGSPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTIISKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	570	97.1	435	10	US-09-932-812-22 Sequence 22, Appl
2	570	97.1	447	10	US-09-968-362-22 Sequence 22, Appl
3	562	95.7	468	14	US-10-071-485-67 Sequence 67, Appl
4	562	95.7	488	12	US-10-683-255-12 Sequence 12, Appl
5	562	95.7	497	12	US-10-683-255-10 Sequence 10, Appl
6	562	95.7	525	12	US-10-683-255-8 Sequence 8, Appl
7	562	95.7	711	14	US-10-071-485-90 Sequence 50, Appl
8	558	95.1	232	14	US-10-008-063-28 Sequence 28, Appl
9	558	95.1	232	14	US-10-008-063-32 Sequence 32, Appl
10	558	95.1	250	14	US-10-152-363A-35 Sequence 35, Appl
11	558	95.1	251	14	US-10-152-363A-31 Sequence 31, Appl
12	558	95.1	251	14	US-10-152-363A-33 Sequence 33, Appl
13	558	95.1	328	14	US-10-008-063-42 Sequence 42, Appl
14	558	95.1	334	14	US-10-152-363A-62 Sequence 62, Appl
15	558	95.1	344	14	US-10-152-363A-52 Sequence 52, Appl

16	558	95.1	348	14	US-10-152-363A-54 Sequence 54, Appl
17	558	95.1	357	14	US-10-152-363A-56 Sequence 56, Appl
18	558	95.1	392	14	US-10-152-363A-50 Sequence 50, Appl
19	558	95.1	437	10	US-09-932-812-20 Sequence 20, Appl
20	558	95.1	449	10	US-09-968-362-20 Sequence 20, Appl
21	558	95.1	473	10	US-09-995-898A-23 Sequence 23, Appl
22	558	95.1	473	12	US-10-420-034A-23 Sequence 23, Appl
23	558	95.1	476	10	US-09-925-055D-23 Sequence 23, Appl
24	558	95.1	476	14	US-10-104-919-62 Sequence 62, Appl
25	558	95.1	476	16	US-10-395-741B-63 Sequence 63, Appl
26	558	95.1	484	10	US-09-925-055D-30 Sequence 30, Appl
27	558	95.1	484	14	US-10-104-919-61 Sequence 61, Appl
28	558	95.1	484	16	US-10-395-741B-62 Sequence 62, Appl
29	558	95.1	559	9	US-09-746-359A-62 Sequence 39, Appl
30	558	95.1	559	12	US-09-951-268-39 Sequence 39, Appl
31	558	95.1	559	15	US-10-424-658-62 Sequence 62, Appl
32	558	95.1	594	9	US-09-746-359A-23 Sequence 23, Appl
33	558	95.1	594	12	US-09-951-268-24 Sequence 24, Appl
34	558	95.1	594	15	US-10-424-658-24 Sequence 24, Appl
35	558	95.1	764	10	US-09-892-949-69 Sequence 69, Appl
36	558	95.1	764	12	US-10-352-554-39 Sequence 39, Appl
37	558	95.1	764	15	US-10-351-157-39 Sequence 39, Appl
38	557	94.9	110	15	US-10-370-749-23 Sequence 23, Appl
39	557	94.9	212	13	US-10-033-522-2 Sequence 2, Appl
40	557	94.9	215	15	US-10-264-049-4290 Sequence 4290, Ap
41	557	94.9	218	12	US-09-813-341-1 Sequence 1, Appl
42	557	94.9	218	12	US-09-813-341-2 Sequence 2, Appl
43	557	94.9	218	14	US-10-277-307-1 Sequence 1, Appl
44	557	94.9	218	14	US-10-277-307-2 Sequence 2, Appl
45	557	94.9	218	14	US-10-277-370-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-932-812-22  
; Sequence 22, Application US/09932812  
; Publication NO. US20030082749A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human erythropoietin with increased biolog  
; FILE REFERENCE: 02SUN2001  
; CURRENT APPLICATION NUMBER: US/09/932,812  
; CURRENT FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 22  
; LENGTH: 435  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuBPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2  
US-09-932-812-22

Query Match	97.1%	Score 570;	DB 10;	Length 435;
Best Local Similarity	97.3%	Pred. No. 1.6e-50;		
Matches 107;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	APPVAGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60		
Db	219	AREVAGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278		
QY	61	PREEQNSTYRVSVTLVTLHQLWLNKGYCKVSNKGLPSSIEKTIISKAK 110		
Db	279	PREEQNSTYRVSVTLVTLHQLWLNKGYCKVSNKGLPSSIEKTIISKAK 328		

RESULT 2  
US-09-968-362-22  
; Sequence 22, Application US/09968362

	Query Match	95.7%	Score 562;	DB 12;	Length 497;
	Best local similarity	95.5%	Pred. No. 1.2e-49;		
	Matches 105;	Conservative	2;	Mismatches 3;	Indels 0;
Qy	1	APPVAGGSPVFPPPKPOTLMISRPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNAKTK	60		
Db	281	APLEGGSPVFPPPKPOTLMISRPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNAKTK	340		



Query Match 95.1%; Score 558; DB 14; Length 232;  
Best Local Similarity 95.5%; Pred. No. 1.3e-49;  
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
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Db 16 APEAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75  
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QY 61 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
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Db 76 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 125  
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RESULT 10  
US-10-152-363A-35  
; Sequence 35, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; APPLICANT: Gross, Jane A.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: 60/293,343  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modified immunoglobulin moiety.  
US-10-152-363A-35

Query Match 95.1%; Score 558; DB 14; Length 250;  
Best Local Similarity 95.5%; Pred. No. 1.4e-49;  
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
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Db 35 APEAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94  
|||

QY 61 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
|||  
Db 95 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 144  
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RESULT 11  
US-10-152-363A-31  
; Sequence 31, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; APPLICANT: Gross, Jane A.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: 60/293,343  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modified immunoglobulin moiety.  
US-10-152-363A-31

Query Match 95.1%; Score 558; DB 14; Length 251;  
Best Local Similarity 95.5%; Pred. No. 2e-49;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
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Db 35 APEAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94  
|||

QY 61 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
|||  
Db 95 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 144  
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RESULT 12  
US-10-152-363A-33  
; Sequence 33, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; APPLICANT: Gross, Jane A.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: 60/293,343  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modified immunoglobulin moiety.  
US-10-152-363A-33

Query Match 95.1%; Score 558; DB 14; Length 251;  
Best Local Similarity 95.5%; Pred. No. 1.4e-49;  
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
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Db 35 APEAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94  
|||

QY 61 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
|||  
Db 95 PREEQNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 144  
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RESULT 13  
US-10-008-063-42  
; Sequence 42, Application US/10008063  
; Publication No. US20030092164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Henne, Randal M.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor  
; FILE REFERENCE: 00-103  
; CURRENT APPLICATION NUMBER: US/10/008,063  
; CURRENT FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Ztnfr12-tcs-Fc5.  
US-10-008-063-42

Query Match 95.1%; Score 558; DB 14; Length 328;  
Best Local Similarity 95.5%; Pred. No. 2e-49;

Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 112 APEAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 171  
QY 61 PREEQYNSTYRVVSVLTVTLHQLWLNKGEYKCKVSNKGLPSSIEKTIISKAK 110  
DB 172 PREEQYNSTYRVVSVLTVTLHQLWLNKGEYKCKVSNKALPSSIEKTIISKAK 221

RESULT 14

US-10-152-363A-62  
; Sequence 62, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; PRIOR FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: 60/293,343  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 62  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion protein.  
US-10-152-363A-62

Query Match 95.1%; Score 558; DB 14; Length 332;  
Best Local Similarity 95.5%; Pred. No. 2e-49;  
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 116 APEAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175  
QY 61 PREEQYNSTYRVVSVLTVTLHQLWLNKGEYKCKVSNKGLPSSIEKTIISKAK 110  
DB 176 PREEQYNSTYRVVSVLTVTLHQLWLNKGEYKCKVSNKALPSSIEKTIISKAK 225

RESULT 15

US-10-152-363A-52  
; Sequence 52, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; PRIOR FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: 60/293,343  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 52  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion protein.  
US-10-152-363A-52

Query Match 95.1%; Score 558; DB 14; Length 344;  
Best Local Similarity 95.5%; Pred. No. 2.1e-49;  
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 128 APEAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 187  
QY 61 PREEQYNSTYRVVSVLTVTLHQLWLNKGEYKCKVSNKGLPSSIEKTIISKAK 110  
DB 188 PREEQYNSTYRVVSVLTVTLHQLWLNKGEYKCKVSNKALPSSIEKTIISKAK 237  
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Job time : 39.5 secs

GenCore version 5.1.6  
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OK: protein - protein search, using sw model

Run on: April 29, 2004, 08:42:33 ; Search time 16.5 Seconds  
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Perfect score: 587  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	562	95.7	488	4	US-09-499-846-12
3	562	95.7	497	4	US-09-499-846-10
4	562	95.7	525	4	US-09-499-846-8
5	562	95.7	711	4	US-09-485-737B-90
6	558	95.1	559	4	US-09-746-359A-62
7	558	95.1	594	4	US-09-746-359A-23
8	557	94.9	110	3	US-08-444-644-21
9	557	94.9	116	2	US-08-232-539D-21
10	557	94.9	212	1	US-08-430-633-4
11	557	94.9	212	2	US-08-620-694A-4
12	557	94.9	212	2	US-08-936-854-4
13	557	94.9	212	3	US-09-022-255-4
14	557	94.9	212	3	US-09-022-696-4
15	557	94.9	212	3	US-09-022-253-4
16	557	94.9	212	3	US-09-022-260-4
17	557	94.9	212	3	US-09-022-259-4
18	557	94.9	212	3	US-09-022-257-4
19	557	94.9	212	4	US-09-549-679-4
20	557	94.9	212	4	US-09-428-082B-2
21	557	94.9	228	4	US-09-847-249A-2
22	557	94.9	229	4	US-09-122-144-2
23	557	94.9	232	2	US-08-595-043A-50
24	557	94.9	235	3	US-09-131-247-6
25	557	94.9	243	4	US-09-428-082B-1068
26	557	94.9	243	4	US-09-428-082B-6
27	557	94.9	247	4	US-09-428-082B-6

28	557	94.9	247	4	US-09-428-082B-12	Sequence 12, Appl
29	557	94.9	248	4	US-09-428-082B-1056	Sequence 1056, Ap
30	557	94.9	248	4	US-09-428-082B-1058	Sequence 1058, Ap
31	557	94.9	248	4	US-09-428-082B-1060	Sequence 1060, Ap
32	557	94.9	248	4	US-09-428-082B-1062	Sequence 1062, Ap
33	557	94.9	250	4	US-09-428-082B-1070	Sequence 1070, Ap
34	557	94.9	252	4	US-09-428-082B-1064	Sequence 1064, Ap
35	557	94.9	252	4	US-09-428-082B-1066	Sequence 1066, Ap
36	557	94.9	253	4	US-09-428-082B-16	Sequence 16, Appl
37	557	94.9	253	4	US-09-428-082B-18	Sequence 18, Appl
38	557	94.9	254	2	US-08-284-331B-33	Sequence 33, Appl
39	557	94.9	254	3	US-09-218-950-33	Sequence 33, Appl
40	557	94.9	268	4	US-09-428-082B-8	Sequence 8, Appl
41	557	94.9	269	4	US-09-428-082B-10	Sequence 10, Appl
42	557	94.9	277	4	US-09-428-082B-20	Sequence 20, Appl
43	557	94.9	277	4	US-09-428-082B-22	Sequence 22, Appl
44	557	94.9	316	3	US-09-178-869-4	Sequence 4, Appli
45	557	94.9	316	4	US-09-761-413-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-485-737B-67  
; Sequence 67, Application US/09485737B  
; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Arge  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; FILE REFERENCE: INNS:015  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-67  
Query Match Similarity 95.7%; Score 562; DB 4; Length 468;  
Best Local Similarity 95.5%; Pred. No. 2.7e-58; Indels 0; Gaps 0;  
Matches 105; Conservative 2; Mismatches 3;  
QY 1 APPVAGGSPVFLPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60  
Db 251 APELLGGPSVFLPPLKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 310  
QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
Db 311 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 360  
RESULT 2  
US-09-499-846-12  
; Sequence 12, Application US/09499846  
; Patent No. 6656728  
; GENERAL INFORMATION:  
; APPLICANT: Kavanaugh et al.  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR  
; FILE REFERENCE: 035784/135012 (5784-

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; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-12

Query Match      95.7%; Score 562; DB 4; Length 488;
Best Local Similarity 95.5%; Pred. No. 2.8e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   ||:|||||
Db 272 APELGGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331
   ||:|||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   ||:|||||
Db 332 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 381
   ||:|||||

RESULT 3
; Sequence 10, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-10

Query Match      95.7%; Score 562; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   ||:|||||
Db 281 APELGGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340
   ||:|||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   ||:|||||
Db 341 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 390
   ||:|||||

RESULT 4
US-09-499-846-8
; Sequence 8, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-8

; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 96/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: BPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: BPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match      95.7%; Score 562; DB 4; Length 711;
Best Local Similarity 95.5%; Pred. No. 4.7e-59;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   ||:|||||
Db 251 APELGGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
   ||:|||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
   ||:|||||
Db 311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 360
   ||:|||||

RESULT 6
US-09-746-359A-62
; Sequence 62, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Egan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
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; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-21
;
; Query Match 94.9%; Score 557; DB 4; Length 110;
; Best Local Similarity 94.5%; Pred. No. 1.5e-58;
; Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
;
; Qy 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
; Db 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
;
; Qy 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
; Db 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110
;
; RESULT 10
; US-08-232-539D-55
; Sequence 55, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-232-539D-55
;
; Query Match 94.9%; Score 557; DB 2; Length 116;
; Best Local Similarity 94.5%; Pred. No. 1.6e-58;
; Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
;
; Qy 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
; Db 6 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
;
; Qy 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
; Db 66 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 115
;
; RESULT 11
; US-08-430-633-4
; Sequence 4, Application US/08430633
; Patent No. 5726286
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus B2LF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,633
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 455
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
;
US-08-620-694A-4

Query Match          94.9%; Score 557; DB 1; Length 212;
Best Local Similarity 94.5%; Pred. No. 3.6e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDITLMSRTPETCVVDVSHEDPEVKFNWYDGVVHNKTK 60
   |||
Db 14 APELLGGPSVFLPPPKDITLMSRTPETCVVDVSHEDPEVKFNWYDGVVHNKTK 73
   |||

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
   |||
Db 74 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 123

RESULT 12
US-08-620-694A-4
; Sequence 4, Application US/08620694A
; Patent No. 5863286
; GENERAL INFORMATION:
; APPLICANT: YAO, ZHENGBIN
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: FANSLAW, WILLIAM
; TITLE OF INVENTION: No. 5863286e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
;
US-08-620-694A-4

Query Match          94.9%; Score 557; DB 2; Length 212;
Best Local Similarity 94.5%; Pred. No. 3.6e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDITLMSRTPETCVVDVSHEDPEVKFNWYDGVVHNKTK 60
   |||
Db 14 APELLGGPSVFLPPPKDITLMSRTPETCVVDVSHEDPEVKFNWYDGVVHNKTK 73
   |||

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
   |||
Db 74 PREEQNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 123

RESULT 13
US-08-936-854-4
; Sequence 4, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFERY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,633
; FILING DATE: 28-APR-1995
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE: Human
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: I9G1 FC
; US-08-936-854-4
;
; Query Match          94.9%; Score 557; DB 2; Length 212;
; Best Local Similarity 94.5%; Pred. No. 3.6e-58;
; Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 APPVAGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
;   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 14 APPELLGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
;
; QY 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTIISKAK 110
;   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 74 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTIISKAK 123
;
; RESULT 14
; US-09-022-255-4
; Sequence 4, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:

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;
; CLONE: I9G1 FC
; US-09-022-255-4
;
; Query Match          94.9%; Score 557; DB 3; Length 212;
; Best Local Similarity 94.5%; Pred. No. 3.6e-58;
; Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 APPVAGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
;   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 14 APPELLGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
;
; QY 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTIISKAK 110
;   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; Db 74 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGLPSSIEKTIISKAK 123
;
; RESULT 15
; US-09-022-696-4
; Sequence 4, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: I9G1 FC
; US-09-022-696-4
;
; Query Match          94.9%; Score 557; DB 3; Length 212;
; Best Local Similarity 94.5%; Pred. No. 3.6e-58;
; Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy	1	APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60
Db	14	APPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	73
Qy	61	PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	110
Db	74	PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	123

Search completed: April 29, 2004, 08:47:43  
Job time : 17.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:33 ; Search time 13.5 Seconds

(without alignments)  
783,783 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583

Sequence: 1 APPVAGGSPVFLPPPKPDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARY5

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	327	1 G4HU	Ig gamma-4 chain C
2	542.5	93.1	326	1 G2HU	Ig gamma-2 chain C
3	541	92.8	234	2 PT0207	Ig gamma chain C r
4	541	92.8	255	4 S31866	Ig gamma-1 chain C
5	541	92.8	330	1 GHU	Ig gamma-1 chain C
6	541	92.8	374	2 S69339	Ig heavy chain V r
7	531	91.1	377	2 A60764	Ig gamma-3 chain C
8	531	91.1	377	2 A23511	Ig gamma-3 chain C
9	518	88.9	289	1 G3HUI	Ig gamma-3 heavy C
10	470	80.6	328	2 I47160	Ig gamma 2b chain
11	470	80.6	328	2 I47159	Ig gamma 2a chain
12	465	79.8	277	2 I47162	Ig gamma 4 chain C
13	443	76.0	328	2 I47161	Ig gamma 3 chain C
14	443	76.0	328	2 I47158	Ig gamma 1 chain C
15	433	74.3	308	2 C30554	Ig heavy chain C r
16	433	74.3	323	1 GHRB	Ig gamma chain C r
17	433	74.3	333	2 PS0018	Ig gamma-2b chain
18	433	74.3	472	2 S31459	Ig gamma-1 chain
19	431	73.9	470	2 S22080	Ig heavy chain pre
20	426	73.1	329	1 G2GP	Ig gamma-2 chain C
21	417	71.5	329	1 G3MSC	Ig gamma-3 chain C
22	417	71.5	398	1 G3MSM	Ig gamma-3 chain C
23	409	70.2	327	2 S06611	Ig gamma-2 chain C
24	405	69.5	324	1 G1MS	Ig gamma-1 chain C
25	405	69.5	393	1 G1MSM	Ig gamma-1 chain C
26	405	69.5	444	2 PC4436	monoclonal antibod
27	403	69.1	329	2 S00847	Ig gamma-2c chain
28	399	68.4	405	1 G2MSB4	Ig gamma-2b chain
29	399	68.4	474	1 G2MS11	Ig gamma-2b chain

RESULT 1  
G4HU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 16-Jul-1999  
C:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Note: The sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30;81-326 <PIN>  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.9%; Score 565; DB 1; Length 327;  
Best Local Similarity 97.3%; Pred. No. 1.2e-48;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	APPVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
Db	111	AREFLGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 170
QY	61	PREEQFNSTYRVVSVLTVHLQDWLNKGYKCKVSNKGLPSSIEKTIKAK 110
Db	171	PREEQFNSTYRVVSVLTVHLQDWLNKGYKCKVSNKGLPSSIEKTIKAK 220

Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-1 chain C  
Ig gamma-2b chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2b chain  
Ig gamma heavy cha  
Ig epsilon-chain  
Ig epsilon chain C  
Ig epsilon chain C  
Ig heavy chain pre  
Ig epsilon chain C

RESULT 2  
G2HU  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000  
C:Accession: A93906; A92809; A93752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6804948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:95066056  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Accession: A92809  
A:Contents: myeloma protein T11  
A:Molecule type: protein  
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:1113060  
A:Accession: A90752  
A:Contents: myeloma protein Zie  
A:Molecule type: protein  
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A:Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation: myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:233-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.1%; Score 542.5; DB 1; Length 326;  
Best Local Similarity 93.6%; Pred. No. 2.1e-46;  
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
QY 1 APPVAGSPVFLPPPKDITLMSIRTPETCVVVDVSOEDPEVQFNWYVDGVEVHNAKTK 60  
Db 111 APPVA-GPSVFLPPPKDITLMSIRTPETCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169  
QY 61 PREEFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
Db 170 PREEFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPAPIEKTISKTK 219  
RESULT 3  
PT0207  
Ig gamma chain C region - chimpanzee  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C:Accession: PT0207  
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A:Reference number: PT0207; MUID:91287716; PMID:2062315  
A:Accession: PT0207  
A:Molecule type: mRNA  
A:Residues: 1-234 <EHR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:48-117/Domain: immunoglobulin homology <IMM>  
Query Match 92.8%; Score 541; DB 2; Length 234;  
Best Local Similarity 91.8%; Pred. No. 2e-46;  
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 APPVAGSPVFLPPPKDITLMSIRTPETCVVVDVSOEDPEVQFNWYVDGVEVHNAKTK 60  
Db 25 APPELLGGSPVFLPPPKDITLMSIRTPETCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 84  
QY 61 PREEFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
Db 85 PREEFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPAPIEKTISKAK 134  
RESULT 4  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:933068; PIDN:CAA49866.1; PID:933069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region  
Query Match 92.8%; Score 541; DB 4; Length 255;  
Best Local Similarity 91.8%; Pred. No. 2.2e-46;  
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 APPVAGSPVFLPPPKDITLMSIRTPETCVVVDVSOEDPEVQFNWYVDGVEVHNAKTK 60  
Db 39 APPELLGGSPVFLPPPKDITLMSIRTPETCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 98  
QY 61 PREEFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
Db 99 PREEFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPAPIEKTISKAK 148

RESULT 5

IGH gamma-1 chain C region - human

C:Species: Homo sapiens (man)  
 C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text\_change 15-Jul-1999  
 C:Accession: A93433; S33861; S33887; B90563; A90564; B91668; A91723; A02146  
 R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
 Nucleic Acids Res. 10, 4071-4079, 1982  
 A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
 A:Reference number: A93433; MUID:82274238; PMID:6287432  
 A:Accession: A93433  
 A:Molecule type: DNA  
 A:Residues: 1-330 <ELL>  
 A:Cross-references: EMBL:217370  
 A>Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers, R:Harris, L.J.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S33904  
 A:Accession: S33861  
 A:Molecule type: DNA  
 A:Residues: 2-330 <HAR>  
 A:Cross-references: EMBL:217370  
 R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.  
 Cell 29, 671-679, 1982  
 A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
 A:Reference number: S33887; MUID:83001943; PMID:6811139  
 A:Accession: S33887  
 A:Molecule type: DNA  
 A:Residues: 88-113,233-330 <PAK>  
 A:Cross-references: EMBL:217370  
 R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B.  
 Biochemistry 9, 3161-3170, 1970  
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
 A:Reference number: A90563; MUID:71064024; PMID:5489771  
 A:Accession: B90563  
 A:Molecule type: protein  
 A:Residues: 1-96, 'R', '98-135 <CUN>  
 A>Note: this sequence has the Gm(3) marker, 97-Arg  
 R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
 Biochemistry 9, 3171-3184, 1970  
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
 A:Reference number: A90564; MUID:71064025; PMID:5530842  
 A:Accession: B90564  
 A:Molecule type: protein  
 A:Residues: 136-154, 'Q', '156-165, 'Q', '167-176, 'Q', '178-194, 'N', '196-197, 'D', '199-238, 'E', '240,  
 A>Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Arg  
 R:Postings, H.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1504, 1976  
 A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
 igen Primärstruktur.  
 A:Reference number: A91668; MUID:77070269; PMID:826475  
 A:Accession: B91668  
 A:Molecule type: protein  
 A:Residues: 1-34, 'Q', '36-96, 'K', '98-115, 'Q', '117-197, 'D', '199-238, 'D', '240, 'L', '242-268, 'E', '27  
 A>Note: this sequence has the Gm(17) and Gm(1) markers  
 R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
 A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO  
 A:Reference number: A91723; MUID:83289131; PMID:6884994  
 A:Accession: B91723  
 A:Molecule type: protein  
 A:Residues: 1-96, 'R', '98-197, 'D', '199-238, 'E', '240, 'W', '242-266, 'D', '268-271, 'D', '273-330 <SCH  
 A>Note: this sequence has the Gm(3) and Gm(non-1) markers  
 R:Gall, W.E.; Edelman, G.M.  
 Biochemistry 9, 3188-3196, 1970  
 A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid

A:Reference number: A90565; MUID:71064027; PMID:4923144

A:Contents: annotation; disulfide bonds  
 R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
 A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunologic  
 endomide cleavage products, and the disulfide bridges.  
 A:Reference number: A91667; MUID:77070267; PMID:1002129

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:137-206/Domain: immunoglobulin homology <IM2>  
 F:243-310/Domain: immunoglobulin homology <IM3>  
 F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
 F:103/Disulfide bonds: interchain (to light chain) #status experimental  
 F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 92.8%; Score 541; DB 1; Length 330;

Best Local Similarity 91.8%; Pred. No. 3e-46; 5; Indels 0; Gaps 0;

Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDITLMSRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 114 APELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 173

QY 61 PREQFNSTYRVSVLTVLDHQLNGKEVCKVNKGIPSSIEKTISKAK 110

DB 174 PREQFNSTYRVSVLTVLDHQLNGKEVCKVNKGIPSSIEKTISKAK 223

RESULT 6

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X81695

R:Khamilchi, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-140, 'C', '142-374 <KH2>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 92.8%; Score 541; DB 2; Length 374;

Best Local Similarity 91.8%; Pred. No. 3.5e-46;

Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDITLMSRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 158 APELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 217

QY 61 PREQFNSTYRVSVLTVLDHQLNGKEVCKVNKGIPSSIEKTISKAK 110



Db 218 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267

RESULT 7

A60764

IG gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A:Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 convert

A:Reference number: A60764; MUID:90007613; PMID:2571587

A:Accession: A60764

A>Status: preliminary

A:Molecule type: DNA

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 531; DB 2; Length 377;

Best Local Similarity 90.0%; Pred. No. 3.5e-45;

Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

Db 161 APPELLGGPSVFLPPLPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 220

QY 61 PREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110

Db 221 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKX 270

RESULT 8

A23511

IG gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c

A:Reference number: A23511; MUID:86148507; PMID:3081877

A:Accession: A23511

A:Molecule type: DNA

C:Cross-references: GS:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056

C:Genetics:

A:Gene: GDB:IGHG3

A:Map position: 14q32.33-14q32.33

A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 531; DB 2; Length 377;

Best Local Similarity 90.0%; Pred. No. 3.5e-45;

Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

Db 161 APPELLGGPSVFLPPLPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 220

QY 61 PREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110

Db 221 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKX 270

RESULT 9

G3H0W1

IG gamma-3 heavy chain disease proteins - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999

C:Accession: A90442; A92219; A90198; A93915; A02149

R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy

A:Reference number: A90442; MUID:81021548; PMID:6774747

A:Contents: heavy chain disease protein Wis

A:Accession: A90442

A:Molecule type: protein

A:Residues: 1-289 <FR>

A>Note: This molecule is a dimer linked by 12 disulfide bonds; it has an extra interchai

A>Note: This protein lacks most of the V region and all of the CHI region. Residue 12 c

A>Note: The sequence of residues 42-76 was taken from the reference that follows

R:Michaelsen, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat

A:Reference number: A92219; MUID:7118561; PMID:402363

A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein

A:Accession: A92219

A:Molecule type: protein

A:Residues: 12-97 <MIC>

A>Note: The hinge region in gamma-3 chains is about four times as long as in other gamm

A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte

R:Wolfsenstein-Tode, C.; Frangione, B.; Prelli, F.; Franklin, E.C.

Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the

A:Reference number: A90198; MUID:77021516; PMID:823945

A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues

A:Accession: A90198

A:Molecule type: protein

A:Residues: 59-125, 128-226, 228-289 <WOL>

A>Note: This protein lacks most of the V region, all of the CHI region, and part of the

R:Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982

A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion

A:Reference number: A93915; MUID:82247835; PMID:6808505

A:Contents: heavy chain disease protein Omm

A:Accession: A93915

A:Molecule type: mRNA

A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-15

A>Note: a carboxyl-terminal lys is removed posttranslationally

A>Note: This sequence may represent an allelic form or another gamma chain subclass

C:Comment: The heavy chain disease protein Wis is shown.

C:Genetics:

A:Gene: GDB:IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid

F;203-270/Domain: immunoglobulin homology <IMM>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 88.9%; Score 518; DB 1; Length 289;

Best Local Similarity 87.3%; Pred. No. 5e-44;

Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

Db 74 APPELLGGPSVFLPPLPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 133

QY 61 PREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110

Db 134 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKX 183

RESULT 10

I47160

IG gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

A:Molecule type: mRNA  
A:Residues: 1-277 <KAC>  
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130  
C:Genetics:  
A:Gene: IG4  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
P;82-151/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 465; DB 2; Length 277;  
Best Local Similarity 80.8%; Pred. No. 8.9e-39;  
Matches 84; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 7 GPSVFLLPPPKDLMISRPEVTCVVVDVSQEDPEVGFYNVYDGVEVHNATKPRREQF 66  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 65 GPSAFIPFPKPDKTLMISRTPKVKVTCVVVDVSQENPEVGFYSWYVDGVEVHTAQTRPKREQF 124  
| | | | | : | | | | | : | | | | | : | | | | |

QY 67 NSTYRVSVSLTVLHODWLNGEKYCKYSNKGLPSSIEKTISKAK 110  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 125 NSTYRVSVSLPIQHODWLNGEKFCKYNNKDLPAPITRIISKAK 168  
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 13

I47161  
IG gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47161  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128  
C:Genetics:  
A:Gene: IG3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
P;133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 443; DB 2; Length 328;  
Best Local Similarity 78.6%; Pred. No. 1.7e-36;  
Matches 81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 7 GPSVFLLPPPKDLMISRPEVTCVVVDVSQEDPEVGFYNVYDGVEVHNATKPRREQF 66  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 116 GPSVFIPFPKPDKTLMISQTPEVTCTVVVDVSKHAEOVFSWYVDGVEVHTAETRPKEQF 175  
| | | | | : | | | | | : | | | | | : | | | | |

QY 67 NSTYRVSVSLTVLHODWLNGEKYCKYSNKGLPSSIEKTISKAK 109  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 176 NSTYRVSVSLPIQHODWLNGEKFCKYNNKDLPAPITRIISKAK 218  
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 14

I47158  
IG gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122  
C:Genetics:  
A:Gene: IG1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
P;133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 443; DB 2; Length 328;  
 Best Local Similarity 78.6%; Pred. No. 1.7e-36;  
 Matches 81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 7 GPSVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVFNAAKTKPREEQF 66  
 DB 116 GPSVFIIPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVFNAAKTKPREEQF 66  
 QY 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKA 109  
 DB 176 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKA 218

# RESULT 15

C30554  
 Ig heavy chain C region - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 03-Mar-1989 #sequence\_revision 03-Mar-1989 #text\_change 21-Jan-2000  
 C:Accession: C30554  
 R:Foley, R.C.; Beh, K.J.  
 J. Immunol. 142, 708-711, 1989  
 A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.  
 A:Reference number: A30554; MUID:89093962; PMID:2492052  
 A:Accession: C30554  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <FOL>  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:113-182/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 433; DB 2; Length 308;  
 Best Local Similarity 71.6%; Pred. No. 1.5e-35;  
 Matches 78; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 2 PPVAGGSPVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVFNAAKTKP 61  
 DB 91 PELGGSPVFIIPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVFNAAKTKP 150  
 QY 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKA 110  
 DB 151 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKA 199

Search completed: April 29, 2004, 08:46:58  
 Job time : 14.5 secs

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:47 ; Search time 10 seconds  
(without alignments)  
572.772 Million cell updates/sec

Title: US-09-674-857-12  
Perfect score: 583  
Sequence: 1 APPVAGGSRVLPFPKPKDT.....CKVSKGLPSSIENTISKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	327	1	GC2_HUMAN
2	542.5	93.1	326	1	GC2_HUMAN
3	541	92.8	330	1	GC1_HUMAN
4	518	88.9	290	1	GC3_HUMAN
5	433	74.3	323	1	GC3_RAT
6	433	74.3	323	1	GC3_RAT
7	426	73.1	329	1	GC2_CAVPO
8	417	71.5	329	1	GC3_MOUSE
9	417	71.5	328	1	GC3_MOUSE
10	405	69.5	344	1	GC1_MOUSE
11	405	69.5	333	1	GC1_MOUSE
12	403	69.1	329	1	GCC_RAT
13	399	68.4	336	1	GC2_MOUSE
14	399	68.4	405	1	GC2_MOUSE
15	396	67.9	335	1	GC2_MOUSE
16	393	67.4	330	1	GC2_MOUSE
17	393	67.4	339	1	GC2_MOUSE
18	389	66.7	326	1	GC1_RAT
19	343	58.8	322	1	GC1_RAT
20	166.5	28.6	428	1	EPC_HUMAN
21	151	25.9	429	1	EPC_RAT
22	151	25.9	457	1	MUC_SUNMU
23	140	24.0	421	1	EPC_MOUSE
24	138.5	23.8	239	1	ALC_RABIT
25	138	23.7	454	1	MUC_HUMAN
26	136	23.3	331	1	MUC_HUMAN
27	133	22.8	106	1	KAC_HUMAN
28	132	22.6	454	1	MUC_MESAU
29	132	22.6	455	1	MUC_MOUSE
30	132	22.6	476	1	MUC_MOUSE
31	128	22.0	103	1	LAC_CHICK
32	125	21.4	450	1	MUC_CANFA
33	125	21.4	458	1	MUC_RABIT

34	125	21.4	479	1	MUCM_RABIT
35	122.5	21.0	105	1	LAC5_MUSSP
36	120.5	20.7	105	1	LAC1_MOUSE
37	120.5	20.7	340	1	ALC2_HUMAN
38	120.5	20.7	353	1	ALC1_GORGO
39	120.5	20.7	353	1	ALC1_HUMAN
40	119.5	20.5	105	1	LAC5_MOUSE
41	114	19.6	103	1	KAC4_RABIT
42	111.5	19.1	344	1	ALC_MOUSE
43	111.5	19.1	393	1	HVC3_HETFR
44	110.5	19.0	213	1	ILL1_HUMAN
45	109.5	18.8	105	1	LAC_HUMAN

ALIGNMENTS

RESULT 1					
GC4_HUMAN	GC4_HUMAN	STANDARD;	PRT;	327 AA.	
ID	AC	P01861;			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Ig gamma-4 chain C region.				
GN	IGHG4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81157104; PubMed=6299562;				
RA	Ellison J.W., Sukbaum J.N., Hood L.E.;				
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";				
RL	DNA 1:11-18(1981).				
RN	[2]				
RP	SEQUENCE OF 1-30 AND 81-326.				
RX	MEDLINE=70207560; PubMed=4192699;				
RA	Pink J.R.L., Buttery S.H., de Vries G.W., Milstein C.;				
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";				
RL	Biochem. J. 117:33-47(1970).				
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CC	-----				
CC	EMBL; K01316; AAB59394.1; ALT_INIT.				
CC	PIR; A90933; G4HU.				
CC	PDB; 1ADQ; 16-SEP-98.				
CC	Genew; HGNC:5528; IGHG4.				
CC	MIM; 147130; .				
CC	GO; GO:0005624; C:membrane fraction; NAS.				
CC	GO; GO:0003823; P:antigen binding; TAS.				
CC	GO; GO:0006955; P:immune response; NAS.				
CC	InterPro; IPR007110; IG-like.				
CC	InterPro; IPR003597; IG_C1.				
CC	InterPro; IPR003006; IG_MHC.				
CC	Pfam; PF00047; Ig; 3.				
CC	SMART; SM00407; IGC1; 2.				
CC	PROSITE; PS50835; IG_LIKE; 3.				
CC	PROSITE; PS00290; IG_MHC; 2.				
KW	Immunoglobulin domain; Immunoglobulin C region; 3D-structure.				
FT	NON_TER 1				
FT	DOMAIN 1 98 CH1.				
FT	DOMAIN 99 110 HINGE.				
FT	DOMAIN 111 220 CH2.				
FT	DOMAIN 221 327 CH3.				

FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 83

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 141 201

FT DISULFID 247 305

SQ SEQUENCE 327 AA; 35940 MW; 35BDB811EF208E7A CRC64;

Query Match 96.98; Score 565; DB 1; Length 327;

Best Local Similarity 97.38; Pred. No. 1.3e-50;

Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSDPEVQFVFNVDGVEVHNATK 60

Db 111 APEFLGGSPVFLPPPKDLMISRTPEVTCVVVDVSDPEVQFVFNVDGVEVHNATK 170

Qy 61 PREQFNSTYRVSVLTVLHQDLNGLNGKEYCKVKNKGLPSISIKTIKAK 110

Db 171 PREQFNSTYRVSVLTVLHQDLNGLNGKEYCKVKNKGLPSISIKTIKAK 220

RESULT 2

ID\_GC2\_HUMAN STANDARD; PRT; 326 AA.

AC P01859;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE IG gamma-2 chain C region.

GN IGHG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE OF 2-326 FROM N.A.

RA MEDLINE=82197621; PubMed=6804948;

PA "Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma

RT heavy chain constant region genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

RP SEQUENCE OF 88-115 FROM N.A.

RC TISSUE=Petal liver;

EX MEDLINE=83001943; PubMed=6811139;

RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;

RT "Structure of human immunoglobulin gamma genes: implications for

RT evolution of a gene family.";

RL Cell 29:671-679(1982).

RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.

RC TISSUE=Petal liver;

EX MEDLINE=84235992; PubMed=6329676;

RA Krawinkel U., Rabbitts T.H.;

RT "Comparison of the hinge-coding segments in human immunoglobulin gamma

RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass

RT genes.";

RL EMBO J. 1:403-407(1982).

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

EX MEDLINE=81007873; PubMed=6774012;

RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic,

RT evolutionary, and functional implications.";

RL J. Immunol. 125:1048-1054(1980).

RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).

EX MEDLINE=80001357; PubMed=113060;

RA Connell G.E., Parr D.M., Hofmann T.;

RT "The amino acid sequences of the three heavy chain constant region

RT domains of a human IgG2 myeloma protein.";

RL Can. J. Biochem. 57:758-767(1979).

RP [6]

RP SEQUENCE OF 238-275 (ZIE).

RX MEDLINE=80114419; PubMed=118920;

RA Hofmann T., Parr D.M.;

RT "A note of the amino acid sequence of residues 381-391 of human

RT immunoglobulins gamma chains.";

RL Mol. Immunol. 16:923-925(1979).

RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).

RA Hofmann T., Parr D.M.;

RL Submitted (MAR-1980) to the PIR data bank.

RP SEQUENCE OF 1-121 (DOT).

RX MEDLINE=95355298; PubMed=7737190;

RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal

RT immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).

RP DISULFIDE BONDS

RX MEDLINE=72033500; PubMed=4940472;

RA Milstein C., Frangione B.;

RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";

RL Biochem. J. 121:217-225(1971).

RP DISULFIDE BONDS

RX MEDLINE=69064124; PubMed=5782707;

RA Frangione B., Milstein C., Pink J.R.L.;

RT "Structural studies of immunoglobulin G.";

RL Nature 221:145-148(1969).

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EMBL: J00230; AAB59393.1; -

PIR: A93906; G2HU

HSP: P01857; IFC1

Genew: HGNC:5526; IGHG2.

MIM: 147110; -

GO: GO:0005624; C:membrane fraction; NAS.

GO: GO:0003823; P:antigen binding; TAS.

GO: GO:0006955; P:immune response; NAS.

InterPro: IPR007110; Ig-like.

InterPro: IPR003597; Ig\_c1.

InterPro: IPR003006; Ig\_MHC.

Pfam: PF00047; Ig; 3.

SMART: SM00407; IGH1; 2.

PROSITE: PS00835; IG\_LIKE; 3.

PROSITE: PS00290; IG\_MHC; 2.

Immunoglobulin domain; Immunoglobulin C region.

NON\_TER 1 1

DOMAIN 1 98 CH1.

DOMAIN 99 110 HINGE.

DOMAIN 111 219 CH2.

DOMAIN 220 326 CH3.

DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).

DISULFID 27 83

DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 140 200

DISULFID 246 304

DISULFID 156 156

SITE 326 326

MOD\_RES 60 60

CONFLICT 109 109

SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

AT OR NEAR THE COMPLEMENT-BINDING SITE.

REMOVED POST-TRANSLATIONALLY (PROBABLE).

S->A (IN MYELOMA PROTEINS TIL & ZIE).

/FTID=VAR\_003889.

C->S (IN REF. 3).

INTERCHAIN (WITH LIGHT CHAIN).

FT	DISULFID	109	109	INTERCHAIN (WITH HEAVY CHAIN).	RP	SEQUENCE (DISEASE PROTEIN WIS).
FT	DISULFID	112	112	INTERCHAIN (WITH HEAVY CHAIN).	RX	MEDLINE=81021548; PubMed=6774747;
FT	DISULFID	144	204		RA	Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
FT	DISULFID	250	308		RT	"Primary structure of human gamma 3 immunoglobulin deletion mutant:
FT	CARBOHYD	180	180	N-LINKED (GLNAC. . .).	RL	gamma 3 heavy-chain disease protein Wis.";
FT	MOD RES	330	330	REMOVED POST-TRANSLATIONALLY.	RN	Biochemistry 19:4304-4308(1980).
FT	VARIANT	97	97	K -> R (IN GIM(3) MARKER).	RP	[2]
FT	VARIANT	239	239	/FTId=VAR_003886.	RP	REVISIONS TO 12-97 (PROTEIN WIS).
FT	VARIANT	241	241	D -> E (IN GIM(NON-1) MARKER).	RA	MEDLINE=77118561; PubMed=402363;
FT	VARIANT	241	241	/FTId=VAR_003887.	RT	Michaelson T.E., Frangione B., Franklin E.C.;
FT	VARIANT	241	241	L -> M (IN GIM(NON-1) MARKER).	RT	"Primary structure of the 'hinge' region of human IgG3. Probable
FT	VARIANT	241	241	/FTId=VAR_003888.	RL	quadruplication of a 15-amino acid residue basic unit.";
FT	STRAND	122	126		RN	J. Biol. Chem. 252:883-889(1977).
FT	HELEX	130	134		RP	[3]
FT	TURN	136	137		RP	REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
FT	TURN	141	147		RX	MEDLINE=77021516; PubMed=823945;
FT	STRAND	141	147		RA	Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
FT	STRAND	157	162		RT	"The amino acid sequence of 'heavy chain disease' protein ZUC.
FT	TURN	163	164		RT	Structure of the FC fragment of immunoglobulin G3.";
FT	STRAND	165	166		RL	Structure of the FC fragment of immunoglobulin G3.";
FT	TURN	168	171		RN	Biochem. Biophys. Res. Commun. 71:907-914(1976).
FT	TURN	176	179		RP	[4]
FT	TURN	180	181		RP	SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
FT	STRAND	182	190		RX	MEDLINE=82247835; PubMed=6808505;
FT	HELEX	193	197		RA	Alexander A., Steinmetz M., Barricault D., Frangione B.,
FT	TURN	198	199		RA	Franklin E.C., Hood L., Buxbaum J.N.;
FT	STRAND	202	207		RT	"Gamma Heavy chain disease in man: cDNA sequence supports partial
FT	TURN	209	210		RT	gene deletion model.";
FT	STRAND	215	219		RL	Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
FT	STRAND	227	227		CC	-!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
FT	STRAND	230	234		CC	interchain disulfide bond at position 7 in addition to the 11
FT	HELEX	238	242		CC	normally present in the hinge region.
FT	STRAND	245	256		CC	-!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
FT	STRAND	260	265		CC	-!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
FT	STRAND	270	270		CC	Ref.2.
FT	STRAND	274	276		CC	-!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
FT	STRAND	280	281		CC	and all of the CH1 region.
FT	TURN	283	284		CC	-!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
FT	STRAND	287	296		CC	of the CH1 region, and part of the hinge compared with normal
FT	HELEX	297	301		CC	gamma-3 heavy chains.
FT	TURN	302	303		CC	-!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
FT	STRAND	305	312		CC	or another gamma chain subclass.
FT	TURN	313	314		CC	-!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
FT	TURN	316	317		CC	times as long as in other gamma chains and contains three
FT	STRAND	320	325		CC	identical 15-residue segments preceded by a similar 17-residue
SQ	SEQUENCE	330 AA;	36106 MW;	3770RE106C2FA33D CRC64;	CC	segment (12-28).
Query Match					CC	-----
Best Local Similarity					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
Matches 101; Conservative					CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
					CC	the European Bioinformatics Institute. There are no restrictions on its
					CC	use by non-profit institutions as long as its content is in no way
					CC	modified and this statement is not removed. Usage by and for commercial
					CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
					CC	or send an email to license@isb-sib.ch).
					CC	-----
Qy	1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSDPEVQFQFNWYDGVGVHNAKTK 60				DR	EMBL; J00231; AAA52805.1; ALT_SEQ.
Ds	114 APELLGGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 173				DR	HSSP; P01857; 1FC1.
Qy	61 PREEQNSTYRVWSVFLVHQQDLNGKEYCKVKNSKGLPSSIKTKSKAK 110				DR	Genew; HGNC:5527; IGHG3.
Ds	174 PREEQNSTYRVWSVFLVHQQDLNGKEYCKVKNSKGLPAPIKTKSKAK 223				DR	MIM; 147120; -.
RESULT 4					DR	GO; GO:0005624; C:membrane fraction; NAS.
ID	GC3 HUMAN				DR	GO; GO:0003823; F:antigen binding; NAS.
AC	P01860;				DR	GO; GO:0006955; P:immune response; NAS.
DT	21-JUL-1986 (Rel. 01, Created)				DR	InterPro; IPR007110; IG-Like.
DT	21-JUL-1986 (Rel. 01, Last sequence update)				DR	InterPro; IPR003597; IG_c1.
DT	15-MAR-2004 (Rel. 43, Last annotation update)				DR	InterPro; IPR003006; IG_MHC.
DE	IG gamma-3 chain C region (Heavy chain disease protein) (HDC).				DR	SMART; SM00407; IGc1; 1.
CN	IGHG3				DR	PROSITE; PS00835; IG_LIKE; 2.
OS	Homo sapiens (Human).				DR	PROSITE; PS00290; IG_MHC; 1.
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				FT	Pyroglutamate carboxylic acid.
OX	NCBI_TaxID=9606;				FT	DOMAIN 12 73 HINGE.
RN	[1]				FT	DOMAIN 74 183 CH2.
					FT	DOMAIN 184 289 CH3.





DB 108 PELGGPSVIFPPKPKDTLMISRTPEVTCVVDVSDDEPEVQFTWVNNQVRTARPL 167

QY 62 REEQFNSTYRVSVLTVLHQQDLNGKEYCKVKVNGKLPSSIEKTIISKAK 110

DB 168 REEQFNSTYRVSVLTPLTHQDLNGKEYCKVKVNGKLPSSIEKTIISKAR 216

RESULT 6

GC\_B\_RAT STANDARD; PRT; 333 AA.

AC G2CB RAT

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE IG gamma-2B chain C region.

OS Rattus norvegicus [rat].

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=9232738; PubMed=3149946;

RA Brueggemann M.;

RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.

DR PIR: PS0018; PS0018.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; Igcl; 2.

DR PROSITE; PS00835; IG\_LIKE; 3.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Repeat.

FT NON TER 1

FT DOMAIN 6 96 IG-LIKE 1.

FT DOMAIN 124 223 IG-LIKE 2.

FT DOMAIN 232 328 IG-LIKE 3.

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 147 207

FT DISULFID 253 311

SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 74.3%; Score 433; DB 1; Length 333;

Best Local Similarity 69.7%; Pred. No. 4.7e-37;

Matches 76; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 2 PPVAGGSPVFLPPKPKDTLMISRTPEVTCVVDVSDDEPEVQFTWVNNQVHNAKTKP 61

DB 118 PELGGPSVIFPPKPKDTLMISRTPEVTCVVDVSDDEPEVQFTWVNNQVHNAKTKP 177

QY 62 REEQFNSTYRVSVLTVLHQQDLNGKEYCKVKVNGKLPSSIEKTIISKAK 110

DB 178 REEQFNSTYRVSVLPIHQDWMGSEKPKCKVNNKALPSPIEKTIISKPK 226

RESULT 7

GC2\_CAVPO STANDARD; PRT; 329 AA.

AC P01862;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-2 chain C region.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

RN [1]

RP SEQUENCE OF 1-3.

RA Trischmann T.M.;

RL Submitted (APR-1975) to the PIR data bank.

RN [2]

RP SEQUENCE OF 4-68.

RP MEDLINE=71058471; PubMed=5538606;

RX Birshstein B.K., Hussain Q.Z., Cebra J.J.;

RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cysteine joining heavy and light chains.";

RL Biochemistry 10:18-25(1971).

RN [3]

RP SEQUENCE OF 69-133 AND 312-329.

RP MEDLINE=71058486; PubMed=5538616;

RA Turner K.J., Cebra J.J.;

RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen bromide fragments.";

RL Biochemistry 10:9-17(1971).

RN [4]

RP SEQUENCE OF 134-226.

RP MEDLINE=75036072; PubMed=4429665;

RA Tracey D.E., Cebra J.J.;

RT "Primary structure of the CH2 homology region from guinea pig IgG2 antibodies.";

RL Biochemistry 13:4796-4803(1974).

RN [5]

RP SEQUENCE OF 227-311.

RP MEDLINE=75036073; PubMed=4609467;

RA Trischmann T.M., Cebra J.J.;

RT "Primary structure of the CH3 homology region from guinea pig IgG2 antibodies.";

RL Biochemistry 13:4804-4811(1974).

RN [6]

RP DISULFIDE BONDS.

RP MEDLINE=71058474; PubMed=4922544;

RA Oliveira B., Lamm M.E.;

RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";

RL Biochemistry 10:26-31(1971).

CC -1- MISCELLANEOUS: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.

DR PIR; A94553; GZGP.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00407; Igcl; 2.

DR PROSITE; PS00835; IG\_LIKE; 3.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

FT NON TER 1

FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 28 79

FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 142 202

FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).

FT DISULFID 248 308

SQ SEQUENCE 329 AA; 35074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 73.1%; Score 426; DB 1; Length 329;

Best Local Similarity 72.5%; Pred. No. 2.4e-36;

Matches 79; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 PPVAGGSPVFLPPKPKDTLMISRTPEVTCVVDVSDDEPEVQFTWVNNQVHNAKTKP 61

DB 113 PELGGPSVIFPPKPKDTLMISRTPEVTCVVDVSDDEPEVQFTWVNNQVHNAKTKP 172

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85027161; PubMed=6092053;  
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
RT Tucker P.W., Blattner F.R.;  
RL "Structural analysis of the murine IgG3 constant region gene.";  
RN EMBO J. 3:2041-2046(1984).  
RP SEQUENCE OF 328-398 FROM N.A.  
RX MEDLINE=84041483; PubMed=6314258;  
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,  
RT Wall R.;  
RL "The structure of the mouse immunoglobulin in gamma 3 membrane gene segment.";  
RN Nucleic Acids Res. 11:6775-6785(1983).  
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DR EMBL; J00451; AAB59655.1; .  
DR EMBL; V01526; CA24767.1; ALT\_SEQ.  
DR PIR; A02156; G3MSW.  
DR HSSP; P01857; IFCL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGc1; 2.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Transmembrane; Alternative splicing.  
FT NON\_TER 1 1  
FT DOMAIN 1 97 CHI.  
FT DOMAIN 98 113 HINGE.  
FT DOMAIN 114 223 CH2.  
FT DOMAIN 224 327 CH3.  
FT TRANSMEM 346 362 POTENTIAL.  
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
FT CONFLICT 333 333 E -> G (IN REF. 2).  
FT CONFLICT 342 342 E -> Q (IN REF. 2).  
FT CONFLICT 388 388 P -> F (IN REF. 2).  
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;  
Query Match 71.5%; Score 417; DB 1; Length 398;  
Best Local Similarity 67.6%; Pred. No. 2e-35;  
Matches 75; Conservative 17; Mismatches 17; Indels 2; Gaps 1;  
QY 2 PP--VAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPPEVQFNWYVDGVEVHNAKT 59  
DB 112 PPGNIGGPSVFIPFPKPKDGLMISLTPEVTCVVVDVSQEDPPEVQFNWYVDGVEVHNAKT 171  
QY 60 KPREEQNSTYRVSVLTVLHODWLNKGYKCKVSKNGLPSSIEKTSKAK 110  
DB 172 QPREAQNSTYRVSVLSALPIQHDWNRGKFKCKVKNKALPAPIERTISKPK 222  
RESULT 10  
GC3M\_MOUSE  
ID GC3M\_MOUSE STANDARD; PRT; 324 AA.  
AC P01868;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)

OY 62 RBEQFNSTYRVSVLTVLHODWLNKGYKCKVSKNGLPSSIEKTSKAK 110  
DB 173 RVEQNTTFRVSVLSALPIQHDWNRGKFKCKVKNKALPAPIERTISKPK 221  
RESULT 8  
GC3M\_MOUSE  
ID GC3M\_MOUSE STANDARD; PRT; 329 AA.  
AC P22436;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-3 chain C region, secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85027161; PubMed=6092053;  
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
RT Tucker P.W., Blattner F.R.;  
RL "Structural analysis of the murine IgG3 constant region gene.";  
RN EMBO J. 3:2041-2046(1984).  
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DR EMBL; J00451; .; NOT\_ANNOTATED\_CDS.  
DR PIR; B02156; G3MSW.  
DR HSSP; P01857; IFCL.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGc1; 2.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Transmembrane; Alternative splicing.  
FT NON\_TER 1 1  
FT DOMAIN 1 97 CHI.  
FT DOMAIN 98 113 HINGE.  
FT DOMAIN 114 223 CH2.  
FT DOMAIN 224 327 CH3.  
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;  
Query Match 71.5%; Score 417; DB 1; Length 329;  
Best Local Similarity 67.6%; Pred. No. 2e-35;  
Matches 75; Conservative 17; Mismatches 17; Indels 2; Gaps 1;  
QY 2 PP--VAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPPEVQFNWYVDGVEVHNAKT 59  
DB 112 PPGNIGGPSVFIPFPKPKDGLMISLTPEVTCVVVDVSQEDPPEVQFNWYVDGVEVHNAKT 171  
QY 60 KPREEQNSTYRVSVLTVLHODWLNKGYKCKVSKNGLPSSIEKTSKAK 110  
DB 172 QPREAQNSTYRVSVLSALPIQHDWNRGKFKCKVKNKALPAPIERTISKPK 222  
RESULT 9  
GC3M\_MOUSE  
ID GC3M\_MOUSE STANDARD; PRT; 398 AA.  
AC P03987;  
DT 23-OCT-1996 (Rel. 02, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-3 chain C region, membrane-bound form.

DE Ig gamma-1 chain C region secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80045036; PubMed=115593;  
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
RA Takahashi N., Mano Y.;  
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
RT gamma 1 chain gene.";  
RL Cell 18:559-568 (1979).  
RN [2]  
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
RX MEDLINE=8020559; PubMed=6769752;  
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
RT cloned in a bacterial plasmid.";  
RL Gene 9:87-97 (1980).  
RN [3]  
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=80012837; PubMed=113776;  
RA Rogers J., Clarke P., Salser W.;  
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
RT heavy chain.";  
RL Nucleic Acids Res. 6:3305-3321 (1979).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=78242288; PubMed=98524;  
RA Adetugbo K.;  
RT "Evolution of immunoglobulin subclasses. Primary structure of a  
RT murine myeloma gamma chain.";  
RL J. Biol. Chem. 253:6068-6075 (1978).  
RN [5]  
RP DISULFIDE BONDS (MOPC 21).  
RX MEDLINE=73008889; PubMed=5073237;  
RA Svasti J., Milstein C.;  
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
RL Biochem. J. 126:837-850 (1972).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Secreted;  
CC IsoId=P01868-1; Sequence=Displayed;  
CC Note=May be the major isoform;  
CC Name=Membrane-bound;  
CC IsoId=P01869-1; Sequence=External;  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; V00793; CAA24172.1; -  
CC EMBL; V00793; CAA24173.1; -  
CC EMBL; V00793; CAA24174.1; -  
CC EMBL; V00793; CAA24175.1; -  
CC EMBL; V00795; CAA24176.1; -  
CC PIR; A02159; GIMS.  
CC GlycoSuiteDB; P01868; -  
CC MGD; MGI:96446; Igh-4.  
CC InterPro; IPR007110; Igh-like.  
CC InterPro; IPR003597; Ig\_c1.  
CC InterPro; IPR003006; Ig\_MHC.  
CC Pfam; PF00447; Igh; 2.  
CC SMART; SM00407; Igc1; 2.  
CC PROSITE; PS00835; IG\_LIKE; 3.  
CC PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing.  
FT NON\_TER 1  
FT DOMAIN 98 CH1.  
FT DOMAIN 110 HINGE.  
FT DOMAIN 111 CH2.  
FT DOMAIN 218 CH3.  
FT DISULFID 27  
FT DISULFID 102 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 104 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 138  
FT CARBOHYD 174 N-LINKED (GLCNAC. . .).  
FT /FTID=CAR\_000055.  
FT DISULFID 244  
FT MOD\_RES 324 REMOVED POST-TRANSLATIONALLY.  
FT CONFLICT 276 N -> D (IN REF. 3).  
FT CONFLICT 278 N -> D (IN REF. 3).  
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
Query Match 69.5%; Score 405; DB 1; Length 324;  
Best Local Similarity 69.6%; Pred. No. 3.4e-34;  
Matches 71; Conservative 18; Mismatches 13; Indels 0; Gaps 0;  
QY 9 SVFLFPKPKDTLMISRTPEVTCVVYVDSQDEPEVFNWYVDGVEVHNKATPREPQFNS 68  
Db 116 SVFIKPKPKDVLITLTPKVTCTVVVDISKDDPEVQSFVDDVEVHTAQTQPREPQFNS 175  
QY 69 TYRVSIVTLVHODWLNKGYCKVKNKGLPSSIRKTSKAK 110  
Db 176 TFRSVSELPIMHODWLNKGYCKVKNKGLPSSIRKTSKAK 217  
RESULT 11  
GC1M\_MOUSE STANDARD; PRT; 393 AA.  
ID GC1M\_MOUSE STANDARD; PRT; 393 AA.  
AC P01869;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig gamma-1 chain C region, membrane-bound form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80045036; PubMed=115593;  
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
RA Takahashi N., Mano Y.;  
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
RT gamma 1 chain gene.";  
RL Cell 18:559-568 (1979).  
RN [2]  
RP SEQUENCE OF 323-393 FROM N.A.  
RX MEDLINE=82197626; PubMed=6804950;  
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;  
RT "mRNA for surface immunoglobulin gamma chains encodes a highly  
RT conserved transmembrane sequence and a 28-residue intracellular  
RT domain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012 (1982).  
RN [3]  
RP SEQUENCE OF 323-366 FROM N.A.  
RX MEDLINE=82115295; PubMed=6799207;  
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
RA Eisenberg D., Wall R.;  
RT "Gene segments encoding transmembrane carboxyl termini of  
RT immunoglobulin gamma chains.";  
RL Cell 26:19-27 (1981).  
RN [4]  
RP SEQUENCE OF 1-44 FROM N.A.  
RX MEDLINE=82222190; PubMed=6283537;

```

RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC CC IsoId=P01869-1; Sequence=Displayed;
CC CC Name=Secreted;
CC CC IsoId=P01868-1; Sequence=External;
CC CC Note=May be the major isoform;
CC -----
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; GIMSM.
DR PDB; 15C8; 23-MAR-99.
DR PDB; 1A56; 18-MAR-98.
DR PDB; 1CL7; 12-JAN-00.
DR PDB; 1F11; 06-FEB-01.
DR PDB; 1F38; 29-DEC-99.
DR PDB; 1KCS; 24-JUL-02.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGI; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane; 3D-structure.
FT NON TER 1 97 CH1.
FT DOMAIN 1 97 HINGE.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 N-LINKED (GLNAC. . .).
FT CARBOHYD 174 174 POTENTIAL.
FT DISULFID 244 302 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 357
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 69.5%; Score 403; DB 1; Length 393;
Best Local Similarity 69.6%; Pred. No. 4.3e-34;
Matches 71; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 9 SVFLPPKPKDITLMIISTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNKTKPRREQFNS 68
DB 116 SVIFPPKPKDITLITLTPKVTCCVVDISKDDPEVQFSNFDVDDVEVHTAQTQPREQFNS 175
QY 69 TYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 176 TFRSSELPIMHQDWLNGKEYKCKVSNKGLPSSIAAPPAIEKTIKTK 217

RESULT 12

```

```

GCC_RAT
ID _GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Bruggemann M., Delmasro-Galfre P., Waldmann H., Calabi P.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3."
RL Eur. J. Immunol. 18:317-319(1988).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -
DR PIR; S00847; S00847.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1 97 CH1.
FT DOMAIN 1 97 HINGE.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 69.1%; Score 403; DB 1; Length 329;
Best Local Similarity 68.6%; Pred. No. 5.6e-34;
Matches 72; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 6 GGPSVFLPPKPKDITLMIISTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNKTKPRREQ 65
DB 118 GRPSVFIPPPKPKDITLITLTPKVTCCVVDVSDQEDPEVQFSNFDVDDVEVHTAQTQPREQ 177
QY 66 FNSYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 178 LMGTRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIAAPPAIEKTIKTKPR 222

RESULT 13
GCC_MOUSE
ID _GCC_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-2B chain C region secreted form.
OS Mus musculus (Mouse).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ALLELE A).  
 RX MEDLINE=60120716; PubMed=6766534;  
 RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;  
 RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene  
 RT cloned from newborn mouse DNA.";  
 RL Nature 283:786-789(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A. (MPC 11).  
 RX MEDLINE=80081501; PubMed=117548;  
 RA Tucker P.W., Marcu K.B., Slignton J.L., Blattner F.R.;  
 RT "Structure of the constant and 3' untranslated regions of the murine  
 RT gamma 2b heavy chain messenger RNA.";  
 RL Science 206:1299-1303(1979).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80081502; PubMed=117549;  
 RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;  
 RT "Sequence of the cloned gene for the constant region of murine gamma  
 RT 2b immunoglobulin heavy chain.";  
 RL Science 206:1303-1306(1979).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ALLELE B).  
 RX MEDLINE=82173203; PubMed=6803173;  
 RA O'Lo R., Rougeon F.;  
 RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma  
 RT 2a and gamma 2b chain genes.";  
 RL Nature 296:761-763(1982).  
 RN [5]  
 RP CARBOHYDRATE-LINKAGE SITE THR-105.  
 RX MEDLINE=94216359; PubMed=7512967;  
 RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,  
 RA Irimura T., Takahashi N., Kato K., Arata Y.;  
 RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";  
 RL J. Biol. Chem. 269:12345-12350(1994).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Secreted;  
 CC IsoId=P01866-1; Sequence=Displayed;  
 CC Note=May be the major isoform;  
 CC Name=Membrane-bound;  
 CC IsoId=P01867-1; Sequence=External;  
 CC -1- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAc DISACCHARIDE WHICH IS  
 CC MODIFIED WITH 2 SIALIC ACID RESIDUES.  
 CC -1- PTM: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA CHAINS.  
 CC -1- MISCELLANEOUS: The a allele sequence is shown.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 DR PIR, S25057; G2MS11.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGC1; 2.  
 DR PROSITE; PS08835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; Repeat.  
 FT NON\_TER 1  
 FT DOMAIN 6 98 IG-LIKE 1.  
 FT DOMAIN 127 226 IG-LIKE 2.  
 FT DOMAIN 235 331 IG-LIKE 3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 150 210

FT DISULFID 256 314 O-LINKED (GALNAc...).  
 FT CARBOHYD 105 105 REMOVED POST-TRANSLATIONALLY (PROBABLE).  
 FT MOD\_RES 336 336 Q -> R (IN ALLELE B).  
 FT VARIANT 163 163 T -> A (IN ALLELE B).  
 FT VARIANT 194 194 N -> D (IN ALLELE B).  
 FT VARIANT 300 300 M -> I (IN ALLELE B).  
 FT VARIANT 301 301 L -> S (IN REF. 2 AND 3).  
 FT CONFLICT 25 25 S -> P (IN REF. 2 AND 3).  
 FT CONFLICT 36 36 I -> T (IN REF. 2 AND 3).  
 FT CONFLICT 239 239  
 SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;  
 Query Match 68.4%; Score 399; DB 1; Length 336;  
 Best Local Similarity 65.5%; Pred. No. 1 Se-33;  
 Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 APPVAGGSPVFLPPPKDMLMISPTPVTVVGVVQSDPEVQFVWYDGVGVHNAKTK 60  
 DB 120 APNLEGGSPVFLPPPKDMLMISPTPVTVVGVVQSDPEVQFVWYDGVGVHNAKTK 179  
 QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKVKYKCKVSKGLPSSIEKTKSKAK 110  
 DB 180 THREDYNSTIRVVSTLPIQHDWMSGRFKCKVNNKDLSPFIERTISKIK 229  
 RESULT 14  
 GCBM MOUSE STANDARD; PRT; 405 AA.  
 AC P01867;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE IG gamma-2B chain C region, membrane-bound form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 335-405 FROM N.A.  
 RX MEDLINE=82222190; PubMed=6283537;  
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
 RT "Nucleotide sequences of gene segments encoding membrane domains of  
 RT immunoglobulin gamma chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
 RN [2]  
 RP SEQUENCE OF 335-378 FROM N.A.  
 RX MEDLINE=82115295; PubMed=6799207;  
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
 RA Eisenberg D., Wall R.;  
 RT "Gene segments encoding transmembrane carboxyl termini of  
 RT immunoglobulin gamma chains.";  
 RL Cell 26:19-27(1981).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Membrane-bound;  
 CC IsoId=P01867-1; Sequence=Displayed;  
 CC Name=Secreted;  
 CC IsoId=P01866-1; Sequence=External;  
 CC Note=May be the major isoform;  
 CC -1- PTM: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA CHAINS.  
 CC -1- MISCELLANEOUS: The sequence of residues 1-335 is assumed to be  
 CC identical with the corresponding region of the secreted form.  
 CC -1- MISCELLANEOUS: The a allele sequence is shown.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
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DR EMBL; J00462; AAB59659.1; ALT_INIT.
DR PIR; C02154; G2MSBM.
DR PDB; 1CIC; 11-MAR-03.
DR MGD; MGI:96445; Igh-3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
KW Alternative splicing; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 127 226 IG-LIKE 2.
FT DOMAIN 235 331 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 150 210 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 256 314 POTENTIAL.
FT TRANSMEM 352 369 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 370 405
FT SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49PA CRC64;

Query Match 68.4%; Score 399; DB 1; Length 405;
Best Local Similarity 65.5%; Pred. No. 1.8e-33;
Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDLMISRPVTCVVVDVSOEDPSVQFNWYVDGVEVHNATK 60
DB 120 APNLEGGSPVFIPFPKIKDVLMSLPKVTCTVVDVSEDDPDVQISWFFVNVVHTAQ 179

QY 61 PREEQNSTYRVSVLTVLHQDLNGLNGKEYCKVKNKGLPSSIEKTIKAK 110
DB 180 THREDYNSTIRVSVLPIQHODWMSCKEKFCKVKNKGLPSPERTISKIK 229

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H.; Bothwell A.L.M.; Mueller-Hill B.; Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2aa and IgG2ab alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J.; Lauwereys M.; Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain FC regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;

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CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -1- MISCELLANEOUS: The sequence differs from that of the a allele,
CC from BALB/c mice, at 15% of the positions.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
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CC
CC EMBL; J00479; -; NOT_ANNOTATED_CDS.
CC PIR; A02153; G2MSAB.
CC PDB; 1BOG; 23-MAR-99.
CC PDB; 1HH6; 26-JAN-01.
CC PDB; 1HH9; 24-JUL-03.
CC PDB; 1HL6; 08-FEB-01.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00407; Igc1; 2.
CC PROSITE; PS00835; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 126 225 IG-LIKE 2.
FT DOMAIN 234 330 IG-LIKE 3.
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 67.9%; Score 396; DB 1; Length 335;
Best Local Similarity 64.5%; Pred. No. 3e-33;
Matches 71; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDLMISRPVTCVVVDVSOEDPSVQFNWYVDGVEVHNATK 60
DB 119 APDLGGSPVFIPFPKIKDVLMSLPKVTCTVVDVSEDDPDVQISWFFVNVVHTAQ 178

QY 61 PREEQNSTYRVSVLTVLHQDLNGLNGKEYCKVKNKGLPSSIEKTIKAK 110
DB 179 THREDYNSTLRVSVLPIQHODWMSCKEKFCKVKNKGLPSPERTISKPR 228

Search completed: April 29, 2004, 08:44:54
Job time : 11 secs

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Db 257 APBFLGSPSVLPPPKPDTLMISRTPEVTCVVVDVSDPEQDFVNWYDGVGVHNAKTK 316
Qy 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110
Db 317 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 366

RESULT 2
Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC051328; AAHS1328.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C8D5B8E12BAAF795C CRC64;

Query Match 92.8%; Score 541; DB 4; Length 469;
Best Local Similarity 91.8%; Pred. No. 1e-52;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPPKPDTLMISRTPEVTCVVVDVSDPEQDFVNWYDGVGVHNAKTK 60
Db 253 APBFLGSPSVLPPPKPDTLMISRTPEVTCVVVDVSDPEQDFVNWYDGVGVHNAKTK 312

Qy 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110
Db 313 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPAPIEKTSKAK 362

RESULT 3
Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC051384; AAHS1384.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 779CF34521483E1A CRC64;

Query Match 92.8%; Score 541; DB 4; Length 470;
Best Local Similarity 91.8%; Pred. No. 1e-52;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPPKPDTLMISRTPEVTCVVVDVSDPEQDFVNWYDGVGVHNAKTK 60
Db 254 APBFLGSPSVLPPPKPDTLMISRTPEVTCVVVDVSDPEQDFVNWYDGVGVHNAKTK 313

Qy 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110
Db 314 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPAPIEKTSKAK 363

RESULT 4
Q72351 PRELIMINARY; PRT; 482 AA.
AC Q72351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein DKFP686N02209.
GN DKFP686N02209.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BX538118; CAD98026.1; -.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
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Query Match          92.8%; Score 541; DB 4; Length 482;
Best Local Similarity 91.8%; Pred. No. 1.le-52;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVHNAKTK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 266 APFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVHNAKTK 325
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 326 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 375
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q96PQ8
ID Q96PQ8 PRELIMINARY; PRT; 679 AA.
AC Q96PQ8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477449; PubMed=11593034;
RA Hu Z.; Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu Z.; Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK58686.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Aa_hydroxyl_S.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR00742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR01314; Peptidase_S1A.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGF; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

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DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match          92.8%; Score 541; DB 4; Length 679;
Best Local Similarity 91.8%; Pred. No. 1.le-52;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVHNAKTK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 463 APFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVHNAKTK 522
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 523 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 572
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q8NF17
ID Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FLJ00385 protein (Fragment).
GN FLJ00385
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H.; Takano J.; Kikuno R.; Nagase T.; Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090464; BAC03445.1; -.
DR PIR; A45874; A45874.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGF1; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON_TER 1
SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match          91.6%; Score 534; DB 4; Length 509;
Best Local Similarity 90.9%; Pred. No. 7.le-52;
Matches 100; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVHNAKTK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 224 APFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVHNAKTK 283
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D6 284 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 333
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q8N4Y9
ID Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR PIR; A60764; A60764.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 91.6%; Score 534; DB 4; Length 521;
Best Local Similarity 90.9%; Pred. No. 7.3e-52;
Matches 100; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 305 APELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 364

OY 61 PREEQNSTYRVSVLTVHLQDWLNKGKEYKCKVSNKGLPSSIEKTIKSKAK 110
DB 365 PREEQNSTYRVSVLTVHLQDWLNKGKEYKCKVSNKGLPSSIEKTIKSKAK 414

RESULT 8
Q86TT2 PRELIMINARY; PRT; 354 AA.
ID Q86TT2
AC Q86TT2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CS01019YF20 of placenta of Homo sapiens
DE (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Gerroscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248278; CAD62606.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Plasmid.
FT NON TER
SQ SEQUENCE 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;
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Query Match 91.1%; Score 531; DB 4; Length 354;
Best Local Similarity 90.0%; Pred. No. 9.9e-52;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 138 APELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 197

OY 61 PREEQNSTYRVSVLTVHLQDWLNKGKEYKCKVSNKGLPSSIEKTIKSKAK 110
DB 198 PREEQNSTYRVSVLTVHLQDWLNKGKEYKCKVSNKGLPSSIEKTIKSKAK 247

RESULT 9
Q95M34 PRELIMINARY; PRT; 337 AA.
ID Q95M34
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EXBL; AJ300875; CAC4624.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON TER
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 79.2%; Score 462; DB 6; Length 337;
Best Local Similarity 74.5%; Pred. No. 6.3e-44;
Matches 82; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 119 APELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 178

OY 61 PREEQNSTYRVSVLTVHLQDWLNKGKEYKCKVSNKGLPSSIEKTIKSKAK 110
DB 179 PREEQNSTYRVSVLTVHLQDWLNKGKEYKCKVSNKGLPSSIEKTIKSKAK 228

RESULT 10
Q7TMK1 PRELIMINARY; PRT; 470 AA.
ID Q7TMK1
AC Q7TMK1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;  
  
Query Match 70.2%; Score 409; DB 11; Length 469;  
Best Local Similarity 70.6%; Pred. No. 9.7e-38;  
Matches 72; Conservative 17; Mismatches 13; Indels 0; Gaps 0;  
  
QY 9 SVFLPPPKDITLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTPRREQFNS 68  
DB 261 SVFIPIPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRREQFNS 320  
QY 69 TVRVSVLTVLHQQDLNGKEYCKVSKNGLPSSIEKTSKAK 110  
DB 321 TFRSVSELPIMHQDLNGKEFKCRVNSAFAPIEKTISKTK 362  
  
RESULT 12  
Q99L1A4 PRELIMINARY; PRT; 437 AA.  
ID Q99L1A4  
AC Q99L1A4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Gammal heavy chain of Mab7 (fragment).  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
RT antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv)".  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152372; AAD40243.1; -  
DR PIR; B45837; B45837.  
DR PDB; 1COK; 11-SEP-99.  
DR PDB; 1I9T; 25-DEC-02.  
DR PDB; 1KCU; 11-MAY-02.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Igh-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1 437  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7B83EE7D697C CRC64;  
  
Query Match 69.5%; Score 405; DB 11; Length 437;  
Best Local Similarity 69.6%; Pred. No. 2.5e-37;  
Matches 71; Conservative 18; Mismatches 13; Indels 0; Gaps 0;  
  
QY 9 SVFLPPPKDITLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTPRREQFNS 68  
DB 229 SVFIPIPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRREQFNS 288  
QY 69 TVRVSVLTVLHQQDLNGKEYCKVSKNGLPSSIEKTSKAK 110  
DB 289 TFRSVSELPIMHQDLNGKEFKCRVNSAFAPIEKTISKTK 330  
  
RESULT 13  
Q99L1A4 PRELIMINARY; PRT; 463 AA.  
ID Q99L1A4  
AC Q99L1A4  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

OX NCBI\_TaxID=10090;  
RN [1]  
SQ SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Breast tumor;  
RX MEDLINE=2238257; PubMed=12477932;  
RA Strausberg R.L., Rainold E.A., Grouse L.H., Dexte J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Wang J., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gharatne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC055910; AAH55910.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51727 MW; 6D9054D5F896BB090 CRC64;  
  
Query Match 71.5%; Score 417; DB 11; Length 470;  
Best Local Similarity 67.6%; Pred. No. 1.2e-38;  
Matches 75; Conservative 17; Mismatches 17; Indels 2; Gaps 1;  
  
QY 2 PF--VAGSPVLPFPKPKDITLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAK 59  
DB 253 PPGNIGSPVLPFPKPKDITLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAK 312  
QY 60 KPREQFNSTVRVSVLTVLHQQDLNGKEYCKVSKNGLPSSIEKTSKAK 110  
DB 313 QPREAQNSTPRVVSALPIQHDWVRGKPKCKVKNKALPAPIRTISKPK 363  
  
RESULT 11  
Q99L3V9 PRELIMINARY; PRT; 469 AA.  
ID Q99L3V9  
AC Q99L3V9  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC024405; AAH24405.1; -  
DR PIR; B45837; B45837.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Igh-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 Similar to RIKEN CDNA 1810060009 gene.  
 IGH-4.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 Strausberg R.;  
 Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL; BC003435; AA03435.1;  
 PIR; B45837; B45837.  
 HSSP; P01842; 7FAB.  
 MGD; MGI:96446; IGH-4.  
 InterPro; IPR007110; Ig-like.  
 InterPro; IPR003006; Ig\_MHC.  
 InterPro; IPR003596; Ig\_V.  
 Pfam; PF00047; Ig\_3.  
 SMART; SM00406; IGV; 1.  
 PROSITE; PS00835; IG LIKE; 4.  
 PROSITE; PS00290; IG\_MHC; 1.  
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 SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;  
 Query Match 69.5%; Score 405; DB 11; Length 463;  
 Best Local Similarity 69.6%; Pred. No. 2.7e-37;  
 Matches 71; Conservative 18; Mismatches 13; Indels 0; Gaps 0;  
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 DB 255 SVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPRREEQFNS 314  
 QY 69 TYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 315 TYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIKAK 356  
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 ID Q91205 PRELIMINARY; PRT; 473 AA.  
 AC Q91205;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN AU044919.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC010327; AA010327.1;  
 DR MGD; MGI:2144967; AU044919.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR000345; Cytochrome\_B.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
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 Query Match 68.4%; Score 399; DB 11; Length 473;  
 Best Local Similarity 65.5%; Pred. No. 1.3e-36;  
 Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 DB 257 APNLEGSPSVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 316  
 QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 317 THREDYNTSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIKAK 366  
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 ID Q9R3H6 PRELIMINARY; PRT; 474 AA.  
 AC Q9R3H6;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN AU044919.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025447; AA025447.1;  
 DR MGD; MGI:2144967; AU044919.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR000345; Cytochrome\_B.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 KW SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;  
 Query Match 68.4%; Score 399; DB 11; Length 474;  
 Best Local Similarity 65.5%; Pred. No. 1.3e-36;  
 Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 DB 258 APNLEGSPSVFLPPKPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 317  
 QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 318 THREDYNTSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTIKAK 367  
 Search completed: April 29, 2004, 08:46:18  
 Job time : 36 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:46:23 ; Search time 38.5 Seconds  
(without alignments)  
791.970 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583  
Sequence: 1 APPVAGGSVFLFPKPKDFT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 27718591 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US05\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	97.8	437	10	US-09-932-812-20
2	570	97.8	449	10	US-09-968-362-20
3	566.5	97.2	472	14	US-10-006-593-67
4	566.5	97.2	472	15	US-10-307-724-67
5	565	96.9	218	12	US-09-813-341-5
6	565	96.9	218	14	US-10-277-307-5
7	565	96.9	218	14	US-10-277-370-5
8	565	96.9	218	14	US-10-196-394-76
9	565	96.9	218	15	US-10-370-749-18
10	565	96.9	284	12	US-10-433-108-24
11	565	96.9	327	9	US-09-925-664-47
12	565	96.9	327	13	US-10-047-542-26
13	565	96.9	327	14	US-10-310-719-7
14	565	96.9	327	14	US-10-112-582-4
15	565	96.9	329	9	US-09-935-868-12

16	565	96.9	329	10	US-09-990-586-100	Sequence 100, Appl
17	565	96.9	329	14	US-10-287-035-12	Sequence 12, Appl
18	565	96.9	329	14	US-10-282-162-12	Sequence 12, Appl
19	565	96.9	329	14	US-10-310-113-169	Sequence 169, Appl
20	565	96.9	329	14	US-10-230-880-100	Sequence 100, Appl
21	565	96.9	382	12	US-10-050-227-7	Sequence 7, Appl
22	565	96.9	382	12	US-10-050-227-10	Sequence 10, Appl
23	565	96.9	396	9	US-09-859-361-2	Sequence 2, Appl
24	565	96.9	396	9	US-09-859-361-5	Sequence 5, Appl
25	565	96.9	417	14	US-10-005-438-2	Sequence 2, Appl
26	565	96.9	443	9	US-09-917-410-4	Sequence 4, Appl
27	565	96.9	444	10	US-09-256-156-4	Sequence 4, Appl
28	565	96.9	448	9	US-09-917-410-6	Sequence 6, Appl
29	565	96.9	465	14	US-10-401-344-2	Sequence 2, Appl
30	565	96.9	467	14	US-10-211-357-8	Sequence 8, Appl
31	565	96.9	467	14	US-10-211-357-10	Sequence 10, Appl
32	565	96.9	467	14	US-10-211-357-12	Sequence 12, Appl
33	565	96.9	467	15	US-10-428-408A-30	Sequence 30, Appl
34	565	96.9	778	9	US-09-935-868-46	Sequence 46, Appl
35	565	96.9	778	9	US-09-935-868-50	Sequence 50, Appl
36	565	96.9	778	14	US-10-287-035-46	Sequence 46, Appl
37	565	96.9	778	14	US-10-287-035-50	Sequence 50, Appl
38	565	96.9	778	14	US-10-287-035-56	Sequence 56, Appl
39	565	96.9	778	14	US-10-287-035-60	Sequence 60, Appl
40	565	96.9	782	9	US-09-935-868-48	Sequence 48, Appl
41	565	96.9	782	9	US-09-935-868-52	Sequence 52, Appl
42	565	96.9	782	14	US-10-287-035-48	Sequence 48, Appl
43	565	96.9	782	14	US-10-287-035-52	Sequence 52, Appl
44	565	96.9	782	14	US-10-287-035-54	Sequence 54, Appl
45	565	96.9	782	14	US-10-287-035-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1  
US-09-932-812-20  
; Sequence 20, Application US/09932812  
; Publication No. US20030082749A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human erythropoietin with increased biolog  
; FILE REFERENCE: 02SUN2001  
; CURRENT APPLICATION NUMBER: US/09/932,812  
; CURRENT FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-VFc gamma4 with a 27-amino acid leader peptide (Figure 2  
; OTHER INFORMATION: )  
US-09-932-812-20

Query Match 97.8%; Score 570; DB 10; Length 437;  
Best Local Similarity 98.2%; Pred. No. 4.8e-50;  
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 APPVAGGSVFLFPKPKDFTLMISGTPEVTCVVDVSOEDPEVQFNMYVDGVEVHNAKTK 60  
221 APEFAGGSVFLFPKPKDFTLMISGTPEVTCVVDVSOEDPEVQFNMYVDGVEVHNAKTK 280  
Db  
QY 61 PREEQFNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTSKAK 110  
281 PREEQFNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTSKAK 330  
Db  
RESULT 2  
US-09-968-362-20

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; Sequence 20, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 449
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vfc gamma4 with a 30-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: B)
US-09-968-362-20

Query Match      97.8%; Score 570; DB 10; Length 449;
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Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
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QY 61 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
DB 293 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 342

RESULT 3
US-10-006-593-67
; Sequence 67, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2000-12-05
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67

Query Match      97.2%; Score 566.5; DB 14; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.2e-49;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 61 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
DB 293 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 315

RESULT 4
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2000-12-05
; PRIOR FILING DATE: 2000-12-05
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

Query Match      97.2%; Score 566.5; DB 15; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.2e-49;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
DB 257 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 315
QY 61 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
DB 316 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 365

RESULT 5
US-09-813-341-5
; Sequence 5, Application US/09813341
; Publication No. US20020004587A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Kathy L.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
; FILE REFERENCE: P1780R1
; CURRENT APPLICATION NUMBER: US/09/813,341
; CURRENT FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-341-5

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Best Local Similarity 97.3%; Pred. No. 6.8e-50;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 2 APEFLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 61

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DB 316 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 365

RESULT 4
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2000-12-05
; PRIOR FILING DATE: 2000-12-05
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

Query Match      97.2%; Score 566.5; DB 15; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.2e-49;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
DB 257 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 315
QY 61 PREEQFNSTYRVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIISKAK 110
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RESULT 5
US-09-813-341-5
; Sequence 5, Application US/09813341
; Publication No. US20020004587A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Kathy L.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
; FILE REFERENCE: P1780R1
; CURRENT APPLICATION NUMBER: US/09/813,341
; CURRENT FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-341-5

Query Match      96.9%; Score 565; DB 12; Length 218;
Best Local Similarity 97.3%; Pred. No. 6.8e-50;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
DB 2 APEFLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 61

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QY 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110  
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RESULT 6

US-10-277-307-5  
; Sequence 5, Application US/10277307  
; Publication No. US20030139908A1  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Glycoprotein Compositions  
; CURRENT APPLICATION NUMBER: US/10/277,307  
; CURRENT FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: US 60/337,642  
; PRIOR FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/347,694  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 9  
; SEQ ID NO 5  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-277-307-5

Query Match 96.9%; Score 565; DB 14; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.8e-50;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 60  
DB 2 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 61  
QY 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110  
DB 62 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 111

RESULT 7

US-10-277-370-5  
; Sequence 5, Application US/10277370  
; Publication No. US20030157108A1  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Glycoprotein Compositions  
; CURRENT APPLICATION NUMBER: US/10/277,370  
; CURRENT FILING DATE: 2003-02-10  
; PRIOR APPLICATION NUMBER: US 60/337,642  
; PRIOR FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/347,694  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 9  
; SEQ ID NO 5  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-277-370-5

Query Match 96.9%; Score 565; DB 14; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.8e-50;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 60  
DB 2 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 61  
QY 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110  
DB 62 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 111

RESULT 8

US-10-196-394-76  
; Sequence 76, Application US/10196394  
; Publication No. US20030171278A1  
; GENERAL INFORMATION:  
; APPLICANT: Mark S. Dennis  
; TITLE OF INVENTION: Compounds that Bind HER2  
; FILE REFERENCE: P1713R1  
; CURRENT APPLICATION NUMBER: US/10/196,394  
; CURRENT FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: US/09/609,721  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/142,232  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 162  
; SEQ ID NO 76  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-196-394-76

Query Match 96.9%; Score 565; DB 14; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.8e-50;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 60  
DB 2 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 61  
QY 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110  
DB 62 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 111

RESULT 9

US-10-370-749-18  
; Sequence 18, Application US/10370749  
; Publication No. US20040002587A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: Fc Region Variants  
; FILE REFERENCE: AMS-07823  
; CURRENT APPLICATION NUMBER: US/10/370,749  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/358,161  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-370-749-18

Query Match 96.9%; Score 565; DB 15; Length 218;  
Best Local Similarity 97.3%; Pred. No. 6.8e-50;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 60  
DB 2 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 61  
QY 61 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 110  
DB 62 PREQFNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTISKAK 111

RESULT 10

US-10-433-108-24  
; Sequence 24, Application US/10433108  
; Publication No. US20040053370A1

GENERAL INFORMATION:  
APPLICANT: LARRICK, JAMES W.  
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
FILE REFERENCE: 030905.0004.CIP1  
CURRENT APPLICATION NUMBER: US/10/047,542  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: PCT/US01/13932  
PRIOR FILING DATE: 2001-04-28  
PRIOR APPLICATION NUMBER: 60/200,298  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 26  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-542-26

Query Match 96.9%; Score 565; DB 13; Length 327;  
Best Local Similarity 97.3%; Pred. No. 1.1e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 111 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170  
QY 61 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
DB 171 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 220

RESULT 13  
US-10-310-719-7  
Sequence 7, Application US/10310719  
Publication No. US20030166163A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
FILE REFERENCE: LEX-020  
CURRENT APPLICATION NUMBER: US/10/310,719  
CURRENT FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 60/337,113  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/371,966  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 7  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
NAME/KEY: misc  
LOCATION: (1)-(327)  
OTHER INFORMATION: Human gamma 4 constant region  
US-10-310-719-7

Query Match 96.9%; Score 565; DB 14; Length 327;  
Best Local Similarity 97.3%; Pred. No. 1.1e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 111 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170  
QY 61 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
DB 171 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 220  
RESULT 14  
US-10-112-582-4

GENERAL INFORMATION:  
APPLICANT: Eli Lilly and Company  
TITLE OF INVENTION: GLP-1 FUSION PROTEINS  
FILE REFERENCE: X-13991  
CURRENT APPLICATION NUMBER: US/10/433,108  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: US 60/251,954  
PRIOR FILING DATE: 2000-06-12  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 24  
LENGTH: 284  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic construct  
US-10-433-108-24

Query Match 96.9%; Score 565; DB 12; Length 284;  
Best Local Similarity 97.3%; Pred. No. 9.3e-50;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 68 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 127  
QY 61 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
DB 128 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 177

RESULT 11  
US-09-925-664-47  
Sequence 47, Application US/09925664  
Patent No. US2002016006A1  
GENERAL INFORMATION:  
APPLICANT: Denney, Jr., Dan W.  
TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia  
FILE REFERENCE: GENITOPE-06499  
CURRENT APPLICATION NUMBER: US/09/925,664  
CURRENT FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/370,453  
PRIOR FILING DATE: 1998-08-09  
PRIOR APPLICATION NUMBER: 08/644,664  
PRIOR FILING DATE: 1996-05-01  
PRIOR APPLICATION NUMBER: 08/761,277  
PRIOR FILING DATE: 1996-12-06  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 47  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-664-47

Query Match 96.9%; Score 565; DB 9; Length 327;  
Best Local Similarity 97.3%; Pred. No. 1.1e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 111 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170  
QY 61 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
DB 171 PREEQNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 220

RESULT 12  
US-10-047-542-26  
Sequence 26, Application US/10047542  
Publication No. US20020168367A1  
GENERAL INFORMATION:



; Sequence 4, Application US/10112582  
; Publication No. US20030166877A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins  
; FILE REFERENCE: LEX-017  
; CURRENT APPLICATION NUMBER: US/10/112,582  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/280,625  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 327  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Ig gamma-4 chain C region  
US-10-112-582-4

Query Match 96.9%; Score 565; DB 14; Length 327;  
Best Local Similarity 97.3%; Pred. No. 1.1e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNNVYDGVVHNATK 60  
DB 111 APEFLGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNNVYDGVVHNATK 170  
QY 61 PREEQNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 171 PREEQNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 220

RESULT 15  
US-09-935-868-12  
; Sequence 12, Application US/09935868  
; Patent No. US20020164690A1  
; GENERAL INFORMATION:  
; APPLICANT: Regeneron Pharmaceuticals, Inc  
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
; FILE REFERENCE: REG 203D  
; CURRENT APPLICATION NUMBER: US/09/935,868  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-868-12

Query Match 96.9%; Score 565; DB 9; Length 329;  
Best Local Similarity 97.3%; Pred. No. 1.1e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNNVYDGVVHNATK 60  
DB 113 APEFLGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNNVYDGVVHNATK 172  
QY 61 PREEQNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 173 PREEQNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 222

Search completed: April 29, 2004, 08:55:55  
Job time : 39.5 secs

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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:42:33 ; Search time 16.5 Seconds  
(without alignments)  
344.173 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583  
Sequence: 1 APPVAGGSPVFLPPPKPDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/8A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/8B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	110	3	US-08-444-644-44
2	565	96.9	110	4	US-08-232-246A-44
3	565	96.9	327	2	US-08-761-277A-47
4	565	96.9	329	4	US-09-313-942-12
5	565	96.9	382	1	US-08-470-299-7
6	565	96.9	382	1	US-08-470-299-10
7	565	96.9	433	5	PCT-US96-13152-4
8	565	96.9	467	1	US-08-704-744-81
9	565	96.9	467	2	US-07-916-098A-45
10	565	96.9	467	3	US-08-523-894-8
11	565	96.9	467	3	US-08-523-894-10
12	565	96.9	467	3	US-08-523-894-12
13	561	96.2	109	2	US-08-070-116A-4
14	561	96.2	109	4	US-08-557-050-4
15	559	95.9	326	3	US-08-808-720-3
16	559	95.9	328	3	US-08-808-720-1
17	559	95.9	331	3	US-08-808-720-5
18	559	95.9	331	3	US-08-808-720-7
19	559	95.9	374	4	US-09-227-595-26
20	559	95.9	374	4	US-09-227-595-28
21	546	93.7	468	4	US-09-485-737B-67
22	546	93.7	488	4	US-09-499-846-12
23	546	93.7	497	4	US-09-499-846-10
24	546	93.7	525	4	US-09-499-846-8
25	546	93.7	711	4	US-09-485-737B-90
26	542.5	93.1	109	3	US-08-444-644-30
27	542.5	93.1	109	4	US-08-232-246A-30

28	542.5	93.1	432	3	US-08-477-460B-2	Sequence 2, Appli
29	542.5	93.1	432	3	US-08-379-516-2	Sequence 2, Appli
30	542.5	93.1	432	3	US-09-329-316-2	Sequence 2, Appli
31	542.5	93.1	432	3	US-08-485-372A-2	Sequence 2, Appli
32	542.5	93.1	432	4	US-09-409-006A-2	Sequence 2, Appli
33	542.5	93.1	432	4	US-08-484-681-2	Sequence 2, Appli
34	542.5	93.1	432	5	PCT-US93-07422-2	Sequence 2, Appli
35	542.5	93.1	451	4	US-09-472-087-70	Sequence 70, Appli
36	542.5	93.1	463	4	US-09-472-087-1	Sequence 1, Appli
37	542.5	93.1	463	4	US-09-472-087-4	Sequence 63, Appli
38	542.5	93.1	463	4	US-09-472-087-63	Sequence 68, Appli
39	542.5	93.1	464	4	US-09-472-087-68	Sequence 2, Appli
40	542.5	93.1	464	4	US-09-472-087-2	Sequence 66, Appli
41	542.5	93.1	464	4	US-09-472-087-66	Sequence 4, Appli
42	542.5	93.1	530	3	US-08-477-460B-4	Sequence 4, Appli
43	542.5	93.1	530	3	US-08-379-516-4	Sequence 4, Appli
44	542.5	93.1	530	3	US-09-329-316-4	Sequence 4, Appli
45	542.5	93.1	530	3	US-08-485-372A-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-08-444-644-44  
; Sequence 44, Application US/08444644  
; Patent No. 6015355  
; GENERAL INFORMATION:  
; APPLICANT: Eriden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Mallia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALX88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-444-644-44

Query Match 96.9%; Score 565; DB 3; Length 110;  
Best Local Similarity 97.3%; Pred. No. 9.6e-61;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 1 APEFLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREQFNSTYRVSVLTFLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110  
DB 61 PREQFNSTYRVSVLTFLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110

RESULT 2  
US-08-232-246A-44  
; Sequence 44, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,246A  
; FILING DATE: 04-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-232-246A-44

Query Match 96.9%; Score 565; DB 4; Length 110;  
Best Local Similarity 97.3%; Pred. No. 9.6e-61;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

DB 1 APEFLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREQFNSTYRVSVLTFLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110  
DB 61 PREQFNSTYRVSVLTFLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110

RESULT 3  
US-08-761-277A-47  
; Sequence 47, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/761,277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENITOPE-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-761-277A-47

Query Match 96.9%; Score 565; DB 2; Length 327;  
Best Local Similarity 97.3%; Pred. No. 4.2e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 111 APEFLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

QY 61 PREQFNSTYRVSVLTFLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110  
DB 171 PREQFNSTYRVSVLTFLHODWLNKGYCKVSNKGLPSSIEKTIKAK 220

RESULT 4  
US-09-313-942-12  
; Sequence 12, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-A

; CURRENT APPLICATION NUMBER: US/09/313,942  
 ; CURRENT FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 09/313,942  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 60/101,858  
 ; PRIOR FILING DATE: 1998-09-25  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 329  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-313-942-12

Query Match 96.9%; Score 565; DB 4; Length 329;  
 Best Local Similarity 97.3%; Pred. No. 4.3e-60;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 APPVAGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 60  
 DB 113 APEFLGGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 172  
 QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 173 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 222

RESULT 5  
 US-08-470-299-7  
 ; Sequence 7, Application US/08470299  
 ; Patent No. 5783181  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Browne, Michael J.  
 ; APPLICANT: Murphy, Kay E.  
 ; APPLICANT: Chapman, Conrad G.  
 ; APPLICANT: Clinkenbeard, Helen E.  
 ; APPLICANT: Young, Peter R.  
 ; APPLICANT: Shatzman, Allan R.  
 ; TITLE OF INVENTION: No. 5783181el Compounds  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road, P.O. Box 1539  
 ; CITY: King of Prussia  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19406  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/470,299  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P31005C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5024  
 ; TELEFAX: 610-270-5090  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 382 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 US-08-470-299-7

Query Match 96.9%; Score 565; DB 1; Length 382;  
 Best Local Similarity 97.3%; Pred. No. 5.2e-60;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 APPVAGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 60  
 DB 166 APEFLGGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 225  
 QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 226 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 275

RESULT 6  
 US-08-470-299-10  
 ; Sequence 10, Application US/08470299  
 ; Patent No. 5783181  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Browne, Michael J.  
 ; APPLICANT: Murphy, Kay E.  
 ; APPLICANT: Chapman, Conrad G.  
 ; APPLICANT: Clinkenbeard, Helen E.  
 ; APPLICANT: Young, Peter R.  
 ; APPLICANT: Shatzman, Allan R.  
 ; TITLE OF INVENTION: No. 5783181el Compounds  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road, P.O. Box 1539  
 ; CITY: King of Prussia  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19406  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/470,299  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P31005C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5024  
 ; TELEFAX: 610-270-5090  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 382 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 US-08-470-299-10

Query Match 96.9%; Score 565; DB 1; Length 382;  
 Best Local Similarity 97.3%; Pred. No. 5.2e-60;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 APPVAGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 60  
 DB 166 APEFLGGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 225  
 QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 226 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 275

Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 APPVAGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 60  
 DB 166 APEFLGGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 225  
 QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 226 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 275

RESULT 6  
 US-08-470-299-10  
 ; Sequence 10, Application US/08470299  
 ; Patent No. 5783181  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Browne, Michael J.  
 ; APPLICANT: Murphy, Kay E.  
 ; APPLICANT: Chapman, Conrad G.  
 ; APPLICANT: Clinkenbeard, Helen E.  
 ; APPLICANT: Young, Peter R.  
 ; APPLICANT: Shatzman, Allan R.  
 ; TITLE OF INVENTION: No. 5783181el Compounds  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road, P.O. Box 1539  
 ; CITY: King of Prussia  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19406  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/470,299  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P31005C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5024  
 ; TELEFAX: 610-270-5090  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 382 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 US-08-470-299-10

Query Match 96.9%; Score 565; DB 1; Length 382;  
 Best Local Similarity 97.3%; Pred. No. 5.2e-60;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 APPVAGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 60  
 DB 166 APEFLGGGSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVENAKTK 225  
 QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 226 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 275

RESULT 7  
 PCT-US96-13152-4  
 ; Sequence 4, Application PC/TUS9613152  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Martin, Ulrich, et al.

```

COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JBO429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
TELEX:
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-744-81

Query Match 96.9%; Score 565; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 6.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDEDPEVFQFNWYVDGVEVHNATK 60
DB 251 APEFLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDEDPEVFQFNWYVDGVEVHNATK 310

QY 61 PREQFNSTYRWSVLTVLHWDLNGKEYCKVSNKGLPSSIEKTIISKAK 110
DB 311 PREQFNSTYRWSVLTVLHWDLNGKEYCKVSNKGLPSSIEKTIISKAK 360

RESULT 9
US-07-916-098A-45
Sequence 45, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: JULY 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

```

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-523-894-8

Query Match 96.9%; Score 565; DB 3; Length 467;  
Best Local Similarity 97.3%; Pred. No. 6.9e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 60  
DB 251 APEFLGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 310  
QY 61 PREQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTISKAK 110  
DB 311 PREQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTISKAK 360

RESULT 11  
US-08-523-894-10  
Sequence 10, Application US/08523894  
Patent No. 6136310  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
APPLICANT: Newman, Roland A.  
APPLICANT: Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
TITLE OF INVENTION: Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-523-894-10

Query Match 96.9%; Score 565; DB 3; Length 467;  
Best Local Similarity 97.3%; Pred. No. 6.9e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 60  
DB 251 APEFLGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 310  
QY 61 PREQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTISKAK 110  
DB 311 PREQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTISKAK 360

RESULT 12

APPLICATION NUMBER: PCT/US91/08843  
FILING DATE: No. 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: No. 5871732ember 27, 1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: JOHN J. MC DONNELL  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,310-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-916-098A-45

Query Match 96.9%; Score 565; DB 2; Length 467;  
Best Local Similarity 97.3%; Pred. No. 6.9e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 60  
DB 252 APEFLGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVVHNATK 311  
QY 61 PREQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTISKAK 110  
DB 312 PREQFNSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTISKAK 361

RESULT 10  
US-08-523-894-8  
Sequence 8, Application US/08523894  
Patent No. 6136310  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
APPLICANT: Newman, Roland A.  
APPLICANT: Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
TITLE OF INVENTION: Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid

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US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Ref, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-SEP-1995
; APPLICATION NUMBER: US/08/523,894
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12

Query Match 96.9%; Score 565; DB 3; Length 467;
Best Local Similarity 97.3%; Pred. No. 6.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGVSFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 251 APEEGGVSFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

QY 61 PREQFNSTYRVSVLTVQLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110
DB 311 PREQFNSTYRVSVLTVQLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 360

RESULT 13
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivlin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: Of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210

US-08-070-116A-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivlin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-JUN-1994
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.

US-08-070-116A-4
; Query Match 96.2%; Score 561; DB 2; Length 109;
; Best Local Similarity 97.2%; Pred. No. 2.9e-60;
; Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPVAGGVSFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
DB 1 PEPFGGVSFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60

QY 62 REEQFNSTYRVSVLTVQLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 110
DB 61 REEQFNSTYRVSVLTVQLHODWLNKGYKCKVSNKGLPSSIEKTSKAK 109

RESULT 14
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivlin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-JUN-1993
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-116A-4
```

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Db      110  AFEPEGAPSVFLFPKPDFTLMSIRPEVTCVVVDVSDQSDPEVQFNWYVDGVEVHNAKTK 169
Qy      61  PREQFNSTYRVYSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db      170  PREQFNSTYRVYSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 219

Search completed: April 29, 2004, 08:47:44
Job time : 17.5 secs

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Search completed: April 29, 2004, 08:47:44  
Job time : 17.5 secs

Qy	2	PPVAGSPSVFLPPPKKOTLMISRTPEVTCVVVDVSQEDPEVQFNMYVDGVEVENAKTKP	61
Db	1	PEFLGGSPSVFLPPPKKOTLMISRTPEVTCVVVDVSQEDPEVQFNMYVDGVEVENAKTKP	60
Qy	62	REEQFNSTYRVYVSVLTVLHQDWLNGKEYCKRVNKGFLPSSIEKTTISKAK	110
Db	61	REEQFNSTYRVYVSVLTVLHQDWLNGKEYCKRVNKGFLPSSIEKTTISKAK	09

Query Match 95.9%; Score 559; DB 3; Length 326;  
Best Local Similarity 96.4%; Pred. No. 2.3e-59;  
Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 APPVAGGPPSVETLFPKPKKDTIMISRTPEVTCVVVDVSOEDPEVFNWYVDGVEVHNAKTK 60